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OM protein - protein search, using sw model

Run on: April 18, 2005, 09:41:10 ; Search time 62 Seconds
(without alignments)
704.902 Million cell updates/sec

Title: US-10-737-208A-1
Perfect score: 595
Sequence: 1 DVVMQTLPLSLPVPCEPAS.....SQSTHVPBLTFGAGTKLELK 113

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04: *
1: Geneseqp1980s: *
2: Geneseqp1990s: *
3: Geneseqp2000s: *
4: Geneseqp2001s: *
5: Geneseqp2002s: *
6: Geneseqp2003as: *
7: Geneseqp2003bs: *
8: Geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	595	100.0	113	8 ADP42956	Adp42956 Humanised
2	595	100.0	220	8 ADP42960	Adp42960 Humanised
3	570	95.8	113	5 AAE27856	Aae27856 Mouse 14.
4	570	95.8	113	5 ADG67528	Adg67528 14.18 ant
5	570	95.8	150	2 AAR11598	Aar11598 Murine mo
6	558	93.8	113	5 AAE27854	Aae27854 Mouse 14.
7	558	93.8	113	5 ADG67526	Adg67526 14.18 ant
8	547	91.9	114	3 AAB21363	Aab21363 Mouse ant
9	532	89.4	113	5 AAE27842	Aae27842 Mouse 14.
10	532	89.4	113	5 ADG67514	Adg67514 14.18 ant
11	530.5	89.2	116	2 AAW71256	Aaw71256 Humanised
12	530.5	89.2	116	2 AAW76126	Aaw76126 Human ICR
13	530.5	89.2	116	2 AAW81450	Aaw81450 Humanised
14	530.5	89.2	116	3 AAY50753	Aay50753 Humanised
15	530.5	89.2	116	3 AAB13046	Aab13046 Protein s
16	530.5	89.2	116	3 AAY82445	Aay82445 Humanised
17	530.5	89.2	116	3 AAU70938	Aau70938 Humanised
18	530.5	89.2	116	7 ADG25716	Adg25716 Humanised
19	530.5	89.2	131	2 AAW34518	Aaw34518 Variable
20	529.5	89.0	111	7 ABR83195	Abr83195 Murine LL
21	529.5	89.0	139	7 ABR82782	Abr82782 Hybridoma
22	529.5	89.0	139	7 ABR82892	Abr82892 Hybridoma
23	529.5	89.0	239	2 AAW71877	Aaw71877 Anti-huma
24	529.5	89.0	239	3 AAB12914	Aab12914 Anti-huma
25	529.5	89.0	253	2 AAR72599	Aar72599 Anti-dans

26	528.5	88.8	113	6 ABB98911	Abb98911 Variable
27	527.5	88.7	144	8 ADM33981	Adm33981 Anti-Nogo
28	527.5	88.7	219	6 ABP96777	Abp96777 TSH recep
29	527.5	88.7	219	6 ABP96778	Abp96778 TSH recep
30	526.5	88.5	133	3 AAY80284	Aay80284 Humanised
31	526.5	88.5	239	2 AAW71876	Aaw71876 Anti-huma
32	526.5	88.5	239	2 AAW71879	Aaw71879 Anti-huma
33	526.5	88.5	239	3 AAB12916	Aab12916 Anti-huma
34	526.5	88.5	239	3 AAB12913	Aab12913 Anti-huma
35	526.5	88.5	251	8 ADP48650	Adp48650 Human L49
36	526.5	88.5	251	8 ADP48656	Adp48656 Human L49
37	526.5	88.5	251	8 ADP48657	Adp48657 Human L49
38	526.5	88.5	251	8 ADP48659	Adp48659 Human L49
39	526.5	88.5	251	8 ADP48661	Adp48661 Human L49
40	526.5	88.5	251	8 ADP48658	Adp48658 Human L49
41	526.5	88.5	251	8 ADP48634	Adp48634 Human L49
42	526.5	88.5	612	8 ADP48636	Adp48636 Human L49
43	526.5	88.5	633	2 AAW87786	Aaw87786 Fusion pr
44	526	88.4	113	5 AAE27852	Aae27852 Mouse 14.
45	526	88.4	113	5 ADG67524	Adg67524 14.18 ant

ALIGNMENTS

RESULT 1

ADP42956
ID ADP42956 standard; protein; 113 AA.

AC ADP42956;

DT 23-SEP-2004 (first entry)

DE Humanised immunoglobulin light chain variable region SEQ ID NO:1.

XX immunoglobulin; variable region; antibody; GD2; cytostatic; gene therapy;
cancer; cell surface glycosphingolipid.

OS Synthetic.

FH Key Location/Qualifiers

FT Region 1..23

FT /label= huVLF1

FT /note= "framework region 1"

FT Region 39..54

FT /label= huVLF2

FT /note= "framework region 2"

FT Region 62..93

FT /label= huVLF3

FT /note= "framework region 3"

FT Region 104..113

FT /label= huVLF4

FT /note= "framework region 4"

WO2004055056-A1.

01-JUL-2004.

16-DEC-2003; 2003WO-EP014295.

17-DEC-2002; 2002US-0433945P.

(MERE) MERCK PATENT GMBH.

Gillies SD, Lo K;

WPI; 2004-488049/46.

PT New modified m14.18 antibodies with reduced immunogenicity and that
specifically bind the human cell surface glycosphingolipid GD2, useful
for treating cancer.

PS Claim 1; SEQ ID NO 1; Sipp; English.

XX The invention relates to a novel antibody variable region, where the
CC antibody variable region specifically binds to human cell surface
CC glycosphingolipid GD2. An antibody variable region of the invention has
CC cytostatic activity, and may have a use in gene therapy. The antibody may
CC be used for treating cancer. The nucleic acid or cell is useful for
CC manufacturing a medicament that may be used for treating diseases such as
CC cancer. The present sequence represents humanised immunoglobulin light
CC chain variable region.
XX Sequence 113 AA;

Query Match 100.0%; Score 595; DB 8; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.3e-43;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DVVMTQTPLSLPVTGEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSRRF 60
DB 1 DVVMTQTPLSLPVTGEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSRRF 60
QY 61 SGVPDRFSGSGGTDTLTKISRVEAEDLGIVYFCSTHVPPLTFGAGTKLELK 113
DB 61 SGVPDRFSGSGGTDTLTKISRVEAEDLGIVYFCSTHVPPLTFGAGTKLELK 113

RESULT 2
ADP42960
ID ADP42960 standard; protein; 220 AA.
AC ADP42960;
XX
DT 23-SEP-2004 (first entry)
XX
DE Humanised immunoglobulin light chain SEQ ID NO:5.
XX
KW immunoglobulin; antibody; GD2; cytostatic; gene therapy; cancer;
KW cell surface glycosphingolipid.
XX
OS Synthetic.
XX
FN WO2004055056-A1.
XX
PD 01-JUL-2004.
XX
PF 16-DEC-2003; 2003WO-EP014295.
XX
PR 17-DEC-2002; 2002US-0433945P.
XX
PA (MERE) MERCK PATENT GMBH.
XX
PI Gillies SD, Lo K;
XX
DR WPI; 2004-488049/46.
DR N-PSDB; ADP42959.
XX
PT New modified m14.18 antibodies with reduced immunogenicity and that
PT specifically bind the human cell surface glycosphingolipid GD2, useful
PT for treating cancer.
XX
PS Disclosure; SEQ ID NO 5; 51pp; English.

XX The invention relates to a novel antibody variable region, where the
CC antibody variable region specifically binds to human cell surface
CC glycosphingolipid GD2. An antibody variable region of the invention has
CC cytostatic activity, and may have a use in gene therapy. The antibody may
CC be used for treating cancer. The nucleic acid or cell is useful for
CC manufacturing a medicament that may be used for treating diseases such as
CC cancer. The present sequence represents humanised immunoglobulin light
CC chain.
XX Sequence 220 AA;

Query Match 100.0%; Score 595; DB 8; Length 220;

Best Local Similarity 100.0%; Pred. No. 2.4e-43;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DVVMTQTPLSLPVTGEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSRRF 60
DB 1 DVVMTQTPLSLPVTGEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSRRF 60
QY 61 SGVPDRFSGSGGTDTLTKISRVEAEDLGIVYFCSTHVPPLTFGAGTKLELK 113
DB 61 SGVPDRFSGSGGTDTLTKISRVEAEDLGIVYFCSTHVPPLTFGAGTKLELK 113

RESULT 3
AAE27856
ID AAE27856 standard; protein; 113 AA.
XX
AC AAE27856;
XX
DT 13-DEC-2002 (first entry)
XX
DE Mouse 14.18 antibody VK region #2.
XX
KW Mouse; fusion protein; immunological; major histocompatibility complex;
KW MHC; gastric upset; nausea; 14.18 antibody.
XX
OS Mus sp.
XX
FN WO200266514-A2.
XX
PD 29-AUG-2002.
XX
PF 18-FEB-2002; 2002WO-EP001690.
XX
PR 19-FEB-2001; 2001EP-00103955.
PR 05-APR-2001; 2001EP-00108291.
XX
PA (MERE) MERCK PATENT GMBH.
XX
PI Gillies S, Carr FJ, Jones T, Carter G, Hamilton A, Williams S;
PI Hanlon M, Watkins J, Baker M, Way JC;
XX
DR WPI; 2002-667054/71.

XX New modified fusion protein with reduced immunogenicity, useful for
PT combining favorable properties of a composition, comprises an
PT immunoglobulin molecule linked to a non-immunoglobulin target
PT polypeptide.

PS Example 19; Page 78; 92pp; English.

XX The invention relates to an immunogenically modified fusion protein
CC derived from a parent fusion protein, comprising first and second
CC proteins/polypeptides, where the first protein is an immunoglobulin
CC molecule or its fragment and the second protein is non-immunoglobulin
CC target polypeptide each linked to the other directly or by a linker
CC molecule. The immunogenically modified fusion protein is useful in
CC combining known favorable properties of a composition or in creating new
CC properties of a composition which elicits biological or pharmacological
CC efficacy without having undesirable physiological effects such as nausea
CC or gastric upset. The present sequence is mouse 14.18 antibody modified
CC epitope. This sequence is used in the exemplification of the invention
XX
SQ Sequence 113 AA;

Query Match 95.8%; Score 570; DB 5; Length 113;
Best Local Similarity 96.5%; Pred. No. 1.8e-41;
Matches 109; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DVVMTQTPLSLPVTGEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSRRF 60
DB 1 DVVMTQTPLSLPVTGEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSRRF 60
QY 61 SGVPDRFSGSGGTDTLTKISRVEAEDLGIVYFCSTHVPPLTFGAGTKLELK 113

Db 61 SGVPRFSGSGGTDFTLKISRVEAEDLGVYFCQSQTHTVPPLTFGAGTKLELK 113
|||||
61 SGVPRFSGSGGTDFTLKISRVEAEDLGVYFCQSQTHTVPPLTFGAGTKLELK 113
|||||

RESULT 4
ADG67528
ID ADG67528 standard; protein; 113 AA.
XX AC
XX ADG67528;
XX
XX 11-MAR-2004 (first entry)
XX
XX 14.18 antibody VK mouse modified epitope.
XX
XX human; mouse; T-cell epitope; major histocompatibility complex; MHC;
KW immunogenicity; MHC class II; antibody.
XX
XX Mus sp.
XX
XX WO200269232-A2.
XX
XX 06-SEP-2002.
XX
XX 18-FEB-2002; 2002WO-EP001688.
XX
XX 19-FEB-2001; 2001EP-00103954.
XX 08-MAR-2001; 2001EP-00105777.
XX 15-MAR-2001; 2001EP-00106536.
XX 15-MAR-2001; 2001EP-00106538.
XX 20-MAR-2001; 2001EP-00106899.
XX 20-MAR-2001; 2001EP-00107012.
XX 27-MAR-2001; 2001EP-00107568.
XX 25-APR-2001; 2001EP-00110220.
XX 30-MAY-2001; 2001EP-00113228.
XX 19-OCT-2001; 2001EP-00124965.
XX 12-NOV-2001; 2001EP-00126859.
XX
XX (MERE) MERCK PATENT GMBH.
XX
XX Carr FJ, Carter G, Jones T, Williams S, Hamilton A;
XX
XX WPI; 2002-750424/81.
XX
XX Identifying potential T-cell epitope peptides within the amino acid
PT sequence of a biological molecule, useful for preparing a biological
PT molecule with reduced immunogenicity, comprises determining peptide
PT binding to MHC molecules.
XX
XX Example 21; Page 67; 85pp; English.
XX
XX The invention relates to a novel method for identifying one or more
CC potential T-cell epitope peptides within the amino acid sequence of a
CC biological molecule by determining the binding of the peptides to major
CC histocompatibility complex (MHC) molecules using in vitro or in silico
CC techniques or biological assays. The method of the invention is useful
CC for preparing a polypeptide, a protein, a fusion protein, an antibody or
CC their fragments with reduced immunogenicity. The potential T-cell epitope
CC peptide within the amino acid sequence of a parent immunogenically non-
CC modified biological molecule identified is useful for preparing a
CC biological molecule with reduced immunogenicity and having a retained
CC desired biological activity, where the T-cell epitope is a 13mer peptide.
XX The present sequence is used in the exemplification of the invention.
XX
XX Sequence 113 AA;
SQ

Query Match 95.8%; Score 570; DB 5; Length 113;
Best Local Similarity 96.5%; Pred. No. 1.8e-41;
Matches 109; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DVVMTQTPSLPVTGEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLHKVSNRF 60
|||||
1 DVVMTQTPSLPVLGDQASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLHKVSNRF 60
|||||

QY 61 SGVPRFSGSGGTDFTLKISRVEAEDLGVYFCQSQTHTVPPLTFGAGTKLELK 113
|||||
Db 61 SGVPRFSGSGGTDFTLKISRVEAEDLGVYFCQSQTHTVPPLTFGAGTKLELK 113
|||||

RESULT 5
AAR11598
ID AAR11598 standard; protein; 150 AA.
XX AC
XX AAR11598;
XX
XX 14-JUN-1991 (first entry)
XX
XX Murine monoclonal 14.18 L chain V region.
XX
XX chimaeric binding protein; immunoglobulin; variable region; mouse;
KW light chain.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
FH Peptide 1..19
FT /label= leader peptide
FT Region 20..120
FT /label= variable region
FT Region 121..132
FT /label= J(kappa5)
FT Region 133..151
FT /label= kappa C region
XX
XX WO9104329-A.
XX
XX 04-APR-1991.
XX
XX 20-SEP-1989; 89US-00409889.
XX
XX 20-SEP-1989; 89US-00409889.
XX
XX (ABBO) ABBOTT LAB.
XX
XX Gillies SD;
XX
XX WPI; 1991-117518/16.
XX N-PSDB; AAQ11292.
XX
XX Fusion protein prodn. - e.g. having dual biological activity, esp.
PT antibodies, by transfecting host cell with constructed cassette and
PT second DNA sequence.
XX
XX Example; Fig 3; 52pp; English.
XX
XX Two separate H and L chain cDNA libraries were prepared from mRNA
CC isolated from the murine hybridoma cell line 14.18. The lambda gt10
CC library was enriched for full-length L- and H-chains. It was screened by
CC filter hybridisation using various C region probes. Ten phage clones from
CC each screening were analysed further by restriction analysis. The L chain
CC cDNA sequence was sequenced and the amino acid sequence deduced from it.
CC It appears to include a 19 amino acid leader followed by sequences that
CC are highly homologous to the anti- GAT family of V(kappa) genes. See also
CC AAQ11291
XX
XX Sequence 150 AA;
SQ

Query Match 95.8%; Score 570; DB 2; Length 150;
Best Local Similarity 96.5%; Pred. No. 2.3e-41;
Matches 109; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DVVMTQTPSLPVTGEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLHKVSNRF 60
|||||
20 DVVMTQTPSLPVLGDQASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLHKVSNRF 79
|||||

QY 61 SGVPRFSGSGGTDFTLKISRVEAEDLGVYFCQSQTHTVPPLTFGAGTKLELK 113
|||||

Db 80 SGVDFRFGSGSGTDFTLKISRVEADLGVYFCQSQSTHVPLTFGAGTKLELK 132

RESULT 6
AAE27854
ID AAE27854 standard; protein; 113 AA.
XX
AC AAE27854;
XX
DT 13-DEC-2002 (first entry)
XX
DE Mouse 14.18 antibody VK region #1.
XX
KW Mouse; fusion protein; immunological; major histocompatibility complex;
MHC; gastric upset; nausea; 14.18 antibody.
XX
OS Mus sp.
XX
PN WO200266514-A2.
XX
PD 29-AUG-2002.
XX
PF 18-FEB-2002; 2002WO-EP001690.
XX
PR 19-FEB-2001; 2001EP-00103955.
XX
PR 05-APR-2001; 2001EP-00108291.
XX
PR (MERE) MERCK PATENT GMBH.
XX
PI Gillies S, Carr FJ, Jones T, Carter G, Hamilton A, Williams S;
PI Hanlon M, Watkins J, Baker M, Way JC;
XX
DR WPI; 2002-667054/71.
XX
PT New modified fusion protein with reduced immunogenicity, useful for
PT combining favorable properties of a composition, comprises an
PT immunoglobulin molecule linked to a non-immunoglobulin target
PT polypeptide.
XX
PS Example 19; Page 78; 92pp; English.
XX
CC The invention relates to an immunogenically modified fusion protein
CC derived from a parent fusion protein, comprising first and second
CC proteins/polypeptides, where the first protein is an immunoglobulin
CC molecule or its fragment and the second protein is non-immunoglobulin
CC target polypeptide each linked to the other directly or by a linker
CC molecule. The immunogenically modified fusion protein is useful in
CC combining known favourable properties of a composition or in creating new
CC properties of a composition which elicits biological or pharmacological
CC efficacy without having undesirable physiological effects such as nausea
CC or gastric upset. The present sequence is mouse 14.18 antibody modified
CC epitope. This sequence is used in the exemplification of the invention
XX
SQ Sequence 113 AA;
Query Match 93.8%; Score 558; DB 5; Length 113;
Best Local Similarity 94.7%; Pred. No. 1.9e-40; Mismatches 4; Indels 0; Gaps 0;
Matches 107; Conservative 2;
QY 1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYHLWYIQKPGQSPKLLIHKVSNNRF 60
Db 1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYHLWYIQKPGQSPKLLIHKVSNNRF 60
QY 61 SGVDFRFGSGSGTDFTLKISRVEADLGVYFCQSQSTHVPLTFGAGTKLELK 113
Db 61 SGVDFRFGSGSGTDFTLKISRVEADLGVYFCQSQSTHVPLTFGAGTKLELK 113

RESULT 7
ADG67526
ID ADG67526 standard; protein; 113 AA.
XX
AC ADG67526;

XX 11-MAR-2004 (first entry)
DT
XX 14.18 antibody VK mouse peptide threaded modified epitope.
DE
XX human; mouse; T-cell epitope; major histocompatibility complex; MHC;
KW immunogenicity; MHC class II; antibody.
XX
OS Mus sp.
XX
PN WO200269232-A2.
XX
PD 06-SEP-2002.
XX
PF 18-FEB-2002; 2002WO-EP001688.
XX
PR 19-FEB-2001; 2001EP-00103954.
PR 08-MAR-2001; 2001EP-00105777.
PR 15-MAR-2001; 2001EP-00106536.
PR 15-MAR-2001; 2001EP-00106538.
PR 20-MAR-2001; 2001EP-00106899.
PR 20-MAR-2001; 2001EP-00107012.
PR 27-MAR-2001; 2001EP-00107568.
PR 25-APR-2001; 2001EP-00110220.
PR 30-MAY-2001; 2001EP-00113228.
PR 19-OCT-2001; 2001EP-00124965.
PR 12-NOV-2001; 2001EP-00126899.
XX
XX (MERE) MERCK PATENT GMBH.
XX
XX Carr FJ, Carter G, Jones T, Williams S, Hamilton A;
PI
XX WPI; 2002-750424/81.
DR
XX
XX Identifying potential T-cell epitope peptides within the amino acid
PT sequence of a biological molecule, useful for preparing a biological
PT molecule with reduced immunogenicity, comprises determining peptide
PT binding to MHC molecules.
XX
PS Example 21; Page 67; 85pp; English.
XX
CC The invention relates to a novel method for identifying one or more
CC potential T-cell epitope peptides within the amino acid sequence of a
CC biological molecule by determining the binding of the peptides to major
CC histocompatibility complex (MHC) molecules using in vitro or in silico
CC techniques or biological assays. The method of the invention is useful
CC for preparing a polypeptide, a protein, a fusion protein, an antibody or
CC their fragments with reduced immunogenicity. The potential T-cell epitope
CC peptide within the amino acid sequence of a parent immunogenically non-
CC modified biological molecule identified is useful for preparing a
CC biological molecule with reduced immunogenicity and having a retained
CC desired biological activity, where the T-cell epitope is a linear peptide.
CC The present sequence is used in the exemplification of the invention.
XX
XX SQ Sequence 113 AA;
Query Match 93.8%; Score 558; DB 5; Length 113;
Best Local Similarity 94.7%; Pred. No. 1.9e-40; Mismatches 4; Indels 0; Gaps 0;
Matches 107; Conservative 2;
QY 1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYHLWYIQKPGQSPKLLIHKVSNNRF 60
Db 1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYHLWYIQKPGQSPKLLIHKVSNNRF 60
QY 61 SGVDFRFGSGSGTDFTLKISRVEADLGVYFCQSQSTHVPLTFGAGTKLELK 113
Db 61 SGVDFRFGSGSGTDFTLKISRVEADLGVYFCQSQSTHVPLTFGAGTKLELK 113

RESULT 8
AAB21363
ID AAB21363 standard; protein; 114 AA.
XX

AC AAB21363;
 XX
 DT 25-JAN-2001 (first entry)
 XX
 DE Mouse antibody 13G9 light chain variable region.
 XX
 KW Mouse; antibody 13G9; antiarthritic; immunosuppressive; neuroprotective;
 KW antiinflammatory; antipsoriatic; interleukin-18; IL-18;
 KW autoimmune disease; multiple sclerosis; rheumatoid arthritis;
 KW type I diabetes; insulin dependent diabetes; IDDM; psoriasis;
 KW inflammatory bowel disease; complementarity determining region; CDR.
 XX
 OS Mus musculus.
 XX
 PN WO200056771-A1.
 XX
 PD 28-SEP-2000.
 XX
 PF 17-MAR-2000; 2000WO-US007349.
 XX
 PR 19-MAR-1999; 99US-0125299P.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Ho YS, Holmes SD, Taylor AH, Abdel-Meguid SS;
 XX
 DR WPI; 2000-628249/60.
 DR N-PSDB; AAA99642.
 XX
 KW Novel anti-human interleukin (IL)-18 rodent neutralizing monoclonal
 PT antibody having high affinity and useful for treating IL-18 mediated
 PT disorders such as multiple sclerosis, rheumatoid arthritis and psoriasis.
 XX
 PS Disclosure; Fig 3; 64pp; English.
 XX
 CC The present sequence is the light chain variable region of the mouse
 CC antibody 13G9. The antibody has high affinity for human interleukin-18
 CC (IL-18) and is useful for treating and diagnosing IL-18-mediated
 CC disorders, e.g. autoimmune diseases such as multiple sclerosis,
 CC rheumatoid arthritis, type I or insulin dependent diabetes, inflammatory
 CC bowel disease and psoriasis. Specific changes can be introduced into the
 CC nucleotide sequences encoding the complementarity determining regions
 CC (CDRs) or framework regions of the variable light chain and heavy chain
 CC peptides. The resulting modified or fusion nucleic acid sequences can
 CC then be introduced into a plasmid for expression
 XX
 SQ Sequence 114 AA;
 Query Match 91.9%; Score 547; DB 3; Length 114;
 Best Local Similarity 92.0%; Pred. No. 1.7e-39;
 Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 QY 1 DVVMTQTPSLPVTGPEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNRF 60
 DB 1 DVVMTQTPSLPVTGPEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNRF 60
 QY 61 SGVPRDFSGSGSGTDFTLKISRVEADLGVYFCQSSTHVPPLTFGGATKLEIK 113
 DB 61 SGVPRDFSGSGSGTDFTLKISRVEADLGVYFCQSSTHVPPLTFGGATKLEIK 113
 RESULT 9
 AAE27842
 ID AAE27842 standard; protein; 113 AA.
 AC AAE27842;
 XX
 DT 13-DEC-2002 (first entry)
 XX
 DE Mouse 14.18 antibody VK modified epitope.
 XX
 KW Mouse; fusion protein; immunological; major histocompatibility complex;
 XX

KW MHC; gastric upset; nausea; 14.18 antibody.
 XX
 OS Mus sp.
 PN WO200266514-A2.
 XX
 PD 29-AUG-2002.
 XX
 PF 18-FEB-2002; 2002WO-EP001690.
 XX
 PR 19-FEB-2001; 2001EP-00103955.
 PR 05-APR-2001; 2001EP-00108291.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Gillies S, Carr FJ, Jones T, Carter G, Hamilton A, Williams S;
 PI Hanlon M, Watkins J, Baker M, Way JC;
 XX
 DR WPI; 2002-667054/71.
 XX
 KW New modified fusion protein with reduced immunogenicity, useful for
 PT combining favorable properties of a composition, comprises an
 PT immunoglobulin molecule linked to a non-immunoglobulin target
 PT polypeptide.
 XX
 PS Example 19; Page 77; 92pp; English.
 XX
 CC The invention relates to an immunogenically modified fusion protein
 CC derived from a parent fusion protein, comprising first and second
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 CC molecule or its fragment and the second protein is non-immunoglobulin
 CC target polypeptide each linked to the other directly or by a linker
 CC molecule. The immunogenically modified fusion protein is useful in
 CC combining known favorable properties of a composition or in creating new
 CC properties of a composition which elicits biological or pharmacological
 CC efficacy without having undesirable physiological effects such as nausea
 CC or gastric upset. The present sequence is mouse 14.18 antibody modified
 CC epitope. This sequence is used in the exemplification of the invention
 XX
 SQ Sequence 113 AA;
 Query Match 89.4%; Score 532; DB 5; Length 113;
 Best Local Similarity 89.4%; Pred. No. 3.3e-38;
 Matches 101; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
 QY 1 DVVMTQTPSLPVTGPEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNRF 60
 DB 1 DVVMTQTPSLPVTGPEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNRF 60
 QY 61 SGVPRDFSGSGSGTDFTLKISRVEADLGVYFCQSSTHVPPLTFGGATKLEIK 113
 DB 61 SGVPRDFSGSGSGTDFTLKISRVEADLGVYFCQSSTHVPPLTFGGATKLEIK 113
 RESULT 10
 ADG67514
 ID ADG67514 standard; protein; 113 AA.
 AC ADG67514;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE 14.18 antibody VK veneered modified epitope.
 XX
 KW human; mouse; T-cell epitope; major histocompatibility complex; MHC;
 KW immunogenicity; MHC class II; antibody.
 XX
 OS Unidentified.
 XX
 PN WO200269232-A2.
 XX
 PD 06-SEP-2002.
 XX

PF 18-FEB-2002; 2002WO-EP001688.
XX 19-FEB-2001; 2001EP-00103954.
PR 08-MAR-2001; 2001EP-00105777.
PR 15-MAR-2001; 2001EP-00106536.
PR 15-MAR-2001; 2001EP-00106538.
PR 20-MAR-2001; 2001EP-00106899.
PR 20-MAR-2001; 2001EP-00107012.
PR 27-MAR-2001; 2001EP-00107568.
PR 25-APR-2001; 2001EP-00110220.
PR 30-MAY-2001; 2001EP-00113428.
PR 19-OCT-2001; 2001EP-00124965.
PR 12-NOV-2001; 2001EP-00126859.
XX (MERE) MERCK PATENT GMEH.
XX Carr FJ, Carter G, Jones T, Williams S, Hamilton A;
XX WPI; 2002-750424/81.
XX
XX Identifying potential T-cell epitope peptides within the amino acid
XX sequence of a biological molecule, useful for preparing a biological
XX molecule with reduced immunogenicity, comprises determining peptide
XX binding to MHC molecules.
XX
XX Example 21; Page 66; 85pp; English.
XX
XX The invention relates to a novel method for identifying one or more
XX potential T-cell epitope peptides within the amino acid sequence of a
XX biological molecule by determining the binding of the peptides to major
XX histocompatibility complex (MHC) molecules using in vitro or in silico
XX techniques or biological assays. The method of the invention is useful
XX for preparing a polypeptide, a protein, a fusion protein, an antibody or
XX their fragments with reduced immunogenicity. The potential T-cell epitope
XX peptide within the amino acid sequence of a parent immunogenically non-
XX modified biological molecule identified is useful for preparing a
XX biological molecule with reduced immunogenicity and having a retained
XX desired biological activity, where the T-cell epitope is a 13mer peptide.
XX The present sequence is used in the exemplification of the invention.
XX
XX SQ Sequence 113 AA;
XX
XX Query Match 89.4%; Score 532; DB 5; Length 113;
XX Best Local Similarity 89.4%; Pred. No. 3.3e-38;
XX Matches 101; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
XX
XX QY 1 DVVMTQPLSLPVTGPEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNRF 60
XX Db 1 DVVMTQSPGTLPSVLSGERATISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNRF 60
XX
XX QY 61 SGVPDRFSGSGGTDFTLTKISRVEAEDLVYFCQSSTHVPPLTFGAGTKLELK 113
XX Db 61 SGVPDRFSGSGGTDFTLTKISRLEAEDLVYFCQSSTHVPPLTFGAGTKLELK 113
XX
XX RESULT 11
XX AAW71256
XX ID AAW71256 standard; protein; 116 AA.
XX AC AAW71256;
XX XX
XX 25-MAR-2003 (revised)
XX 18-NOV-1998 (first entry)
XX
XX Humanised murine antibody ICR-8.1 light chain amino acid sequence.
XX
XX Human; ICAM-R; intercellular adhesion molecule; adhesion; treatment;
XX inflammatory condition; asthma; tumour growth; metastasis;
XX viral infection; antibody ICR-8.1.
XX
XX Synthetic.
XX Mus sp.
XX Homo sapiens.

XX US5811517-A.
XX 22-SEP-1998.
XX
XX 07-JUN-1995; 95US-00483389.
XX
XX 27-JAN-1992; 92US-00827689.
XX 26-MAY-1992; 92US-00889724.
XX 05-JUN-1992; 92US-00894061.
XX 22-JAN-1993; 93US-00009266.
XX 26-JAN-1993; 93WO-US000787.
XX 05-AUG-1993; 93US-00102852.
XX 05-AUG-1994; 94US-00286754.
XX (ICOS-) ICOS CORP.
XX
XX Vazeux R, Gallatin WM;
XX
XX WPI; 1998-530940/45.
XX N-PSDB; AAV54860.
XX
XX DNA encoding mutant ICAM-R poly:peptide(s) - useful for diagnosis and
XX treatment of cell adhesion based disease conditions e.g. inflammation or
XX asthma.
XX
XX Example 13; Col 119-122; 11lpp; English.
XX
XX The present sequence represents the humanised light chain of murine
XX antibody ICR-8.1. This antibody is specific for ICAM-R (intercellular
XX adhesion molecule-R). ICAMs are polypeptides that are expressed on blood
XX vessel endothelial cell surfaces and are involved in the adhesion events
XX in various conditions. ICAM-R variants (see AAW1264-69) can be used to
XX treat or monitor inflammatory conditions involving specific or
XX nonspecific immune responses, asthma, tumour growth and/or metastasis and
XX viral infections. The ICAM variants are produced recombinantly, from
XX expression libraries of mutated sequences, and the ones that are claimed
XX are the ones that have been found to be especially involved in adhesion
XX events. They can also be used to raise antibodies, also for use as
XX therapeutic or diagnostic agents. (Updated on 25-MAR-2003 to correct PR
XX field.)
XX
XX SQ Sequence 116 AA;
XX
XX Query Match 89.2%; Score 530.5; DB 2; Length 116;
XX Best Local Similarity 88.5%; Pred. No. 4.5e-36;
XX Matches 100; Conservative 9; Mismatches 3; Indels 1; Gaps 1;
XX
XX QY 1 DVVMTQPLSLPVTGPEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNRF 60
XX Db 5 DIVMTQSPSLPVTGPEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPQLLIYKVNRF 64
XX
XX QY 61 SGVPDRFSGSGGTDFTLTKISRVEAEDLVYFCQSSTHVPPLTFGAGTKLELK 113
XX Db 65 SGVPDRFSGSGGTDFTLTKISRVEAEDLVYFCQSSTHVPPLTFGAGTKVEIK 116
XX
XX RESULT 12
XX AAW76126
XX ID AAW76126 standard; protein; 116 AA.
XX AC AAW76126;
XX XX
XX 20-NOV-1998 (first entry)
XX
XX Human ICR-8.1 V-K region PCR product protein.
XX
XX Intercellular adhesion molecule; human; ICAM-R; modulator; 14.3.3 family;
XX HSI-beta; tubulin; inhibitor; stimulator; effector; immune response;
XX inflammation; disorder; T cell activation; macrophage; Crohn's disease;
XX adult respiratory distress syndrome; stroke; multiple sclerosis; asthma;
XX rheumatoid arthritis; tumour growth; human immune deficiency virus;
XX infection; diabetes; graft vs. host disease; passive immunisation.

Db 65 SGVDRFSGSGTDFLKISRVEADVGYICQSSTHV-PYTFGQTKVEIK 116

Search completed: April 18, 2005, 10:00:56
Job time : 65 secs

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A;Title: Active site structure and antigen binding properties of idiotypically cross-reactive antibodies
A;Reference number: A34903; MUID:50094387; PMID:2104617

A;Accession: G34903
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-131 <BED>
A;Cross-references: GB:M32381; GB:J05237; GB:J05238; NID:G639654; PIDN:AAA61588.1; PID:G639654
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;35-114/Domain: immunoglobulin homology <IMM>

Query Match 90.0%; Score 535.5; DB 2; Length 131;
Best Local Similarity 92.0%; Pred. No. 2e-42;
Matches 104; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 DVVMTQPLSLPVTGEPASISCRSSQSLVHRNGNTYHLWYLOKPGQSPKLLIHKVSRRF 60
DB 20 DVVMTQPLSLPVTGEPASISCRSSQSLVHRNGNTYHLWYLOKPGQSPKLLIHKVSRRF 79
QY 61 SGVPRDFSGSGTDFTLKISRVEADLGIVFCSQSTHVPPLTFGAGTKLELK 113
DB 80 SGVPRDFSGSGTDFTLKISRVEADLGIVFCSQSTHVPPLTFGAGTKLELK 131

RESULT 3

IG kappa chain precursor V region (IDB5.7) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: PT0178
R;Perfetti, V.; Borden, P.; Tao, M.H.; Morrison, S.L.; Kabat, E.A.
Mol. Immunol. 28, 505-515, 1991
A;Title: Specificity and variable region cDNA sequence of an isogenic monoclonal anti-idiotypic antibody
A;Reference number: PT0174; MUID:91287738; PMID:1712074

A;Accession: PT0178
A;Molecule type: mRNA
A;Residues: 1-131 <PER>
A;Cross-references: UNIPROT:Q8VC16
A;Experimental source: strain BALB/c
C;Comment: IDB5.7 is an antibody to anti-alpha (1-6) dextran.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;35-114/Domain: immunoglobulin homology <IMM>

Query Match 90.0%; Score 535.5; DB 2; Length 131;
Best Local Similarity 92.9%; Pred. No. 2e-42;
Matches 105; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

QY 1 DVVMTQPLSLPVTGEPASISCRSSQSLVHRNGNTYHLWYLOKPGQSPKLLIHKVSRRF 60
DB 20 DVVMTQPLSLPVTGEPASISCRSSQSLVHRNGNTYHLWYLOKPGQSPKLLIHKVSRRF 79
QY 61 SGVPRDFSGSGTDFTLKISRVEADLGIVFCSQSTHVPPLTFGAGTKLELK 113
DB 80 SGVPRDFSGSGTDFTLKISRVEADLGIVFCSQSTHVPPLTFGAGTKLELK 131

RESULT 4

IG kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C;Accession: S38715
R;Cimani, A.Y.
submitted to the EMBL Data Library, November 1993

A;Reference number: S38713
A;Accession: S38715
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-115 <CIM>
A;Cross-references: EMBL:X76015; NID:G416094; PIDN:CAA53602.1; PID:G1334077
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

F;19-98/Domain: immunoglobulin homology <IMM>

Query Match 89.3%; Score 531.5; DB 2; Length 115;
Best Local Similarity 90.3%; Pred. No. 4.2e-42;
Matches 102; Conservative 6; Mismatches 4; Indels 1; Gaps 1;

QY 1 DVVMTQPLSLPVTGEPASISCRSSQSLVHRNGNTYHLWYLOKPGQSPKLLIHKVSRRF 60
DB 4 DVVMTQPLSLPVTGEPASISCRSSQSLVHRNGNTYHLWYLOKPGQSPKLLIHKVSRRF 63
QY 61 SGVPRDFSGSGTDFTLKISRVEADLGIVFCSQSTHVPPLTFGAGTKLELK 113
DB 64 SGVPRDFSGSGTDFTLKISRVEADLGIVFCSQSTHVPPLTFGAGTKLELK 115

RESULT 5

IG kappa chain precursor V region (MRL10) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 04-May-1989 #sequence_revision 04-May-1989 #text_change 09-Jul-2004
C;Accession: B30577
R;Kofler, R.; Noonan, D.J.; Levy, D.E.; Wilson, M.C.; Moller, N.P.H.; Dixon, F.J.; Theofilopoulos, A.N.; et al.
J. Exp. Med. 161, 805-815, 1985
A;Title: Genetic elements used for a murine lupus anti-DNA autoantibody are closely related to those of the murine anti-DNA autoantibody
A;Reference number: A30577; MUID:85159423; PMID:3920343

A;Accession: B30577
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-131 <KOF>
A;Cross-references: UNIPROT:Q8VC16
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;35-114/Domain: immunoglobulin homology <IMM>

Query Match 89.2%; Score 530.5; DB 2; Length 131;
Best Local Similarity 91.2%; Pred. No. 5.9e-42;
Matches 103; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 1 DVVMTQPLSLPVTGEPASISCRSSQSLVHRNGNTYHLWYLOKPGQSPKLLIHKVSRRF 60
DB 20 DVVMTQPLSLPVTGEPASISCRSSQSLVHRNGNTYHLWYLOKPGQSPKLLIHKVSRRF 79
QY 61 SGVPRDFSGSGTDFTLKISRVEADLGIVFCSQSTHVPPLTFGAGTKLELK 113
DB 80 SGVPRDFSGSGTDFTLKISRVEADLGIVFCSQSTHVPPLTFGAGTKLELK 131

RESULT 6

IG kappa chain V region (H146-24B3) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 21-Jan-2000
C;Accession: E27887
R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A;Title: Structural and functional implications of a restricted antibody response to a dextran antigen
A;Reference number: A91043; MUID:86300658; PMID:2427335

A;Accession: E27887
A;Molecule type: DNA
A;Residues: 1-112 <CAT>
A;Experimental source: strain Balb/c
A;Note: This sequence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus h
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 89.0%; Score 529.5; DB 2; Length 112;
Best Local Similarity 91.2%; Pred. No. 6.2e-42;
Matches 103; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 1 DVVMTQPLSLPVTGEPASISCRSSQSLVHRNGNTYHLWYLOKPGQSPKLLIHKVSRRF 60
DB 4 DVVMTQPLSLPVTGEPASISCRSSQSLVHRNGNTYHLWYLOKPGQSPKLLIHKVSRRF 63

C:Species: Mus musculus (house mouse)
C:Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 21-Jul-2000
C:Accession: B34904; H34903
R:Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A:Title: Active site structure and antigen binding properties of idiotypically cross-re-
A:Reference number: A34903; MUID:90094387; PMID:2104617
A:Accession: B34904
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-131 <BED>
A:Cross-references: GB:M32384; GB:J05237; GB:J05238; NID:9639656; PIDN:AAA61589.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:35-114/Domain: immunoglobulin homology <IMM>

Query Match 88.8%; Score 528.5; DB 2; Length 131;
Best Local Similarity 91.2%; Pred. No. 9e-42; Mismatches 4; Indels 1; Gaps 1;
Matches 103; Conservative

Qy 1 DVVMTQPLSLPVTGPEPASISCRSSQSLVHNGNTYLHWYLPKQSPKLLIHKVSNRF 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 DVVMTQPLSLPVLGDAQSISCRSSQSLVHNGNTYLHWYLPKQSPKLLIHKVSNRF 79
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 SGVPDRFSSGGSGTDFTLKISRVEAEDLGVYFCQSSTHVPTFGAGTKLELK 113
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 SGVPDRFSSGGSGTDFTLKISRVEAEDLGVYFCQSSTHVPTFGAGTKLEIK 131
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 10
PL0205
anti-DNA autoantibody BV16-19, kappa chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: PL0205
R:Smith, R.G.; Voss Jr., E.W.
Mol. Immunol. 27, 463-470, 1990
A:Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from
A:Reference number: PL0198; MUID:90309768; PMID:2114528
A:Accession: PL0205
A:Molecule type: mRNA
A:Residues: 1-113 <SMI>
A:Cross-references: GB:X53645; NID:G50194; PIDN:CAA37696.1; PID:G930140
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-95/Domain: immunoglobulin homology <IMM>
F:24-39/Region: complementarity-determining 1
F:55-61/Region: complementarity-determining 2
F:94-102/Region: complementarity-determining 3
F:101-113/Region: JH region

Query Match 88.7%; Score 527.5; DB 2; Length 113;
Best Local Similarity 92.0%; Pred. No. 9.5e-42; Mismatches 3; Indels 1; Gaps 1;
Matches 104; Conservative

Qy 1 DVVMTQPLSLPVTGPEPASISCRSSQSLVHNGNTYLHWYLPKQSPKLLIHKVSNRF 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DVVMTQPLSLPVLGDAQSISCRSSQSLVHNGNTYLHWYLPKQSPKLLIHKVSNRF 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 SGVPDRFSSGGSGTDFTLKISRVEAEDLGVYFCQSSTHVPTFGAGTKLELK 113
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SGVPDRFSSGGSGTDFTLKISRVEAEDLGVYFCQSSTHVPTFGAGTKLEIK 112
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 11
PL0257
Ig kappa chain V region (anti-DNA, Dp1VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
C:Accession: PL0257
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, J.
J. Exp. Med. 171, 285-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A:Reference number: PL0231; MUID:90111618; PMID:2104919

A;Accession: PL0257
A;Molecule type: mRNA
A;Residues: 1-111 <SHL>
A;Cross-references: UNIPROT:Q8VCI6
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-95/Domain: immunoglobulin homology <IMM>
F;24-39/Region: complementarity-determining 1
F;40-54/Region: framework 2
F;55-61/Region: complementarity-determining 2
F;62-93/Region: framework 3
F;94-102/Region: complementarity-determining 3
F;103-111/Region: framework 4

Query Match 88.3%; Score 525.5; DB 2; Length 111;
Best Local Similarity 91.1%; Pred. No. 1.4e-41;
Matches 102; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

QY 1 DVVMTQTPSLPVTGEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNRF 60
DB 1 DVVMTQTPSLPVTGEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNRF 60

QY 61 SGVDPFRFSGSGGTDFTLKISRVEAEDLGVYFCQSSTHVPPLTFGAGTKLEL 112
DB 61 SGVDPFRFSGSGGTDFTLKISRVEAEDLGVYFCQSSTHVPPLTFGAGTKLEI 111

RESULT 12
B27887
Ig kappa chain V region (H37-62) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
C;Accession: B27887
R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
A;Title: Structural and functional implications of a restricted antibody response to a
A;Reference number: A91043; MUID:86300658; PMID:2427335
A;Accession: B27887
A;Molecule type: DNA
A;Residues: 1-112 <CAT>
A;Cross-references: UNIPROT:Q8VCI6
A;Experimental source: strain Balb/c
A;Note: This sequence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus H
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 88.3%; Score 525.5; DB 2; Length 112;
Best Local Similarity 89.4%; Pred. No. 1.4e-41;
Matches 101; Conservative 6; Mismatches 5; Indels 1; Gaps 1;

QY 1 DVVMTQTPSLPVTGEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNRF 60
DB 1 DVVMTQTPSLPVTGEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNRF 60

QY 61 SGVDPFRFSGSGGTDFTLKISRVEAEDLGVYFCQSSTHVPPLTFGAGTKLEL 113
DB 61 SGVDPFRFSGSGGTDFTLKISRVEAEDLGVYFCQSSTHVPD-TFGGKTLEIK 112

RESULT 13
B32513
Ig kappa chain precursor V region (MRL4) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C;Accession: B32513
R;Kotler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;
J. Clin. Invest. 82, 852-860, 1988
A;Title: Immunoglobulin kappa light chain variable region gene complex organization and
A;Reference number: A94689; MUID:88331394; PMID:3138286
A;Accession: B32513

A;Molecule type: DNA
A;Residues: 1-131 <KOF>
A;Cross-references: GB:M20828; NID:g196937; PIDN:AAA38843.1; PID:g196938
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;35-114/Domain: immunoglobulin homology <IMM>

Query Match 88.2%; Score 524.5; DB 2; Length 131;
Best Local Similarity 90.3%; Pred. No. 2.1e-41;
Matches 102; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 1 DVVMTQTPSLPVTGEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNRF 60
DB 20 DVVMTQTPSLPVTGEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNRF 79

QY 61 SGVDPFRFSGSGGTDFTLKISRVEAEDLGVYFCQSSTHVPPLTFGAGTKLEL 113
DB 80 SGVDPFRFSGSGGTDFTLKISRVEAEDLGVYFCQSSTHVP-PYTFGSGTKLEIK 131

RESULT 14
C34904
Ig kappa chain precursor V region (3-24) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 09-Jul-2004
C;Accession: C34904; I31485
J;Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A;Title: Active site structure and antigen binding properties of idiotypically cross-re
A;Reference number: A34903; MUID:90094387; PMID:2104617
A;Accession: C34904
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-131 <BED>
A;Cross-references: UNIPROT:Q8VCI6
J;Bedzyk, W.D.; Johnson, L.S.; Riordan, G.S.; Voss Jr., E.W.
J. Biol. Chem. 264, 1565-1569, 1989
A;Title: Comparison of variable region primary structures within an anti-fluorescein idi
A;Reference number: A31485; MUID:89109167; PMID:2492278
A;Accession: I31485
A;Status: preliminary
A;Molecule type: protein
A;Residues: 20-52 <BB2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;35-114/Domain: immunoglobulin homology <IMM>

Query Match 88.2%; Score 524.5; DB 2; Length 131;
Best Local Similarity 90.3%; Pred. No. 2.1e-41;
Matches 102; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY 1 DVVMTQTPSLPVTGEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNRF 60
DB 20 DVVMTQTPSLPVTGEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNRF 79

QY 61 SGVDPFRFSGSGGTDFTLKISRVEAEDLGVYFCQSSTHVPPLTFGAGTKLEL 113
DB 80 SGVDPFRFSGSGGTDFTLKISRVEAEDLGVYFCQSSTHVP-PYTFGSGTKLEIK 131

RESULT 15
S32189
Ig kappa chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Accession: S32189
R;Izui, S.
submitted to the EMBL Data Library, February 1993
A;Reference number: S32185
A;Accession: S32189
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-112 <IZU>

A;Cross-references: EMBL:X70094; NID:g288255; PIDN:CAA49699.1; PID:g288256
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 88.0%; Score 523.5; DB 2; Length 112;
Best Local Similarity 90.3%; Pred. No. 2.2e-41;
Matches 102; Conservative 4; Mismatches 6; Indels 1; Gaps 1;
QY 1 DVVMTOTPLSLPVTGPEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNRF 60
Db 1 DVVMTYPLSLPVS LGDQASISCRSSQSLVHSGNTYLHWYLOKPGQSPKLLIHKVSNRF 60
QY 61 SGVPDRFSGSGGCTDFTLKISRVEAEDLGVYFCQSQTHV-PYTFGGGTKLEIK 113
Db 61 SGVPDRFSGSGGCTDFTLKISRVEAEDLGVYFCQSQTHV-PYTFGGGTKLEIK 112

Search completed: April 18, 2005, 10:06:46
Job time : 11.5 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 09:42:15 ; Search time 84.5 Seconds
(without alignments)
684.792 Million cell updates/sec

Title: US-10-737-208A-1
Perfect score: 595
Sequence: 1 DVVMTQTPLSLPTGEPAS.....SQSTHVPPLTFGAGTKLELK 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	518.5	87.1	113	1	KV2G_MOUSE	P01631 mus musculus
2	494.5	83.1	219	2	Q652C0	Q652C0 mus musculus
3	491.5	82.6	248	2	Q652Q7	Q652Q7 mus sp. b3
4	465	78.2	240	2	Q6PIH6	Q6PIH6 homo sapien
5	464	78.0	114	2	Q9UL80	Q9UL80 homo sapien
6	463.5	77.9	113	1	KV2D_HUMAN	P01617 homo sapien
7	462.5	77.7	239	2	Q8TCD0	Q8TCD0 homo sapien
8	455.5	76.6	239	2	Q6P491	Q6P491 homo sapien
9	453.5	76.2	117	1	KV2E_HUMAN	P06309 homo sapien
10	453.5	76.2	133	1	KV2F_HUMAN	P06310 homo sapien
11	452.5	76.1	239	2	Q8NEK0	Q8NEK0 homo sapien
12	444	74.6	115	1	KV2A_HUMAN	P01614 homo sapien
13	440.5	74.0	113	1	KV2B_HUMAN	P01615 homo sapien
14	426	71.6	112	1	KV2C_HUMAN	P01616 homo sapien
15	416.5	70.0	113	1	KV2F_MOUSE	P01630 mus musculus
16	411.5	69.2	113	1	KV2E_MOUSE	P013976 mus musculus
17	396.5	66.6	112	1	KV2D_MOUSE	P01629 mus musculus
18	396.5	66.6	112	2	Q6LEW8	Q6LEW8 mus musculus
19	396.5	66.6	113	1	KV2C_MOUSE	P01628 mus musculus
20	395.5	66.5	112	1	KV2A_MOUSE	P01626 mus musculus
21	384	64.5	108	1	KV1_CANFA	P01618 canis famul
22	379	63.7	255	2	Q6KE05	Q6KE05 mus musculus
23	358	60.2	120	1	KV2B_MOUSE	P01627 mus musculus
24	355.5	59.7	133	1	KV4B_HUMAN	P06313 homo sapien
25	354	59.5	111	1	KV3N_MOUSE	P01666 mus musculus
26	354	59.5	111	1	KV3S_MOUSE	P01671 mus musculus
27	353	59.3	111	1	KV3U_MOUSE	P01673 mus musculus
28	353	59.3	134	1	KV4C_HUMAN	P06314 homo sapien
29	351	59.0	114	1	KV4A_HUMAN	P01625 homo sapien
30	350	58.8	262	2	Q652I1	Q652I1 mus musculus
31	349.5	58.7	112	1	KV3B_MOUSE	P01655 mus musculus

32	349	58.7	86	2	Q7Z3Y5	Q7Z3Y5 homo sapien
33	349	58.7	111	1	KV3H_MOUSE	P01660 mus musculus
34	349	58.7	236	2	Q6PII8	Q6PII8 homo sapien
35	346	58.2	111	1	KV3K_MOUSE	P01663 mus musculus
36	345.5	58.1	109	2	Q9UL78	Q9UL78 homo sapien
37	345	58.0	111	1	KV3M_MOUSE	P01665 mus musculus
38	344	57.8	111	1	KV3T_MOUSE	P01672 mus musculus
39	343	57.6	111	1	KV3O_MOUSE	P01667 mus musculus
40	343	57.6	111	2	Q920E9	Q920E9 mus musculus
41	342.5	57.6	109	1	KV3D_HUMAN	P01622 homo sapien
42	342.5	57.6	110	1	KV3P_MOUSE	P01668 mus musculus
43	342	57.5	111	1	KV3R_MOUSE	P01670 mus musculus
44	341.5	57.4	235	2	Q6GMV9	Q6GMV9 homo sapien
45	341	57.3	111	1	KV3L_MOUSE	P01664 mus musculus

ALIGNMENTS

RESULT 1
KV2G_MOUSE STANDARD; PRT; 113 AA.
AC P01631;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region 26-10.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=83178921; PubMed=6404298;
RA Novotny J., Margolies M.N.;
RT "Amino acid sequence of the light chain variable region from a mouse
anti-digoxin hybridoma antibody.";
RL Biochemistry 22:1153-1158(1983).
CC -1- MISCELLANEOUS: This chain was isolated from an IGG2a hybridoma
protein that binds digoxin.
DR PIR; A01914; KVM526.
DR HSSP; Q99M37; I191.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig_1.
DR SMART; SM00406; IGV; 1.
KW PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Hybridoma; Immunoglobulin V region;
KW Monoclonal antibody.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 39 Complementarity-determining-1.
FT DOMAIN 40 54 Framework-2.
FT DOMAIN 55 61 Complementarity-determining-2.
FT DOMAIN 62 93 Framework-3.
FT DOMAIN 94 102 Complementarity-determining-3.
FT DOMAIN 103 112 Framework-4.
FT DISULFID 23 93 By similarity.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;

Query Match 87.1%; Score 518.5; DB 1; Length 113;
Best Local Similarity 88.5%; Pred. No. 2.4e-46;
Matches 100; Conservative 7; Mismatches 5; Indels 1; Gaps 1;

QY	1	DVVM	QTPLSLPTGEPASISCRSSQSLVHRNGNTYLHWYLOKPOQSKLLIHKVS	NRFP 60
Db	1	DVVM	QTPLSLPTGEPASISCRSSQSLVHRNGNTYLHWYLOKPOQSKLLIHKVS	NRFP 60
QY	61	SGVDP	RFSGSGTGFTLKSIVEADLGVYFCSQSTHYVPLTFGAGTKLELK	113
Db	61	SGVDP	RFSGSGTGFTLKSIVEADLGVYFCSQSTHYVPLTFGAGTKLELK	112

```
RESULT 2
Q652C0 PRELIMINARY; PRT; 219 AA.
ID Q652C0
AC Q652C0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Kappa light chain C region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/c; TISSUE=Spleen;
RA MEDLINE=96319505; PubMed=8768802;
RX Kipp B., Schlaak M., Becker W.M.;
RT "Cloning and expression of a recombinant mouse Fab-fragment
RT recognizing a defined linear epitope of Chironomus thummi major
RT allergen Chi t I."
RL Int. Arch. Allergy Immunol. 110:348-353 (1996).
DR EMBL; Z37499; CAA85724.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00230; IG_MHC; UNKNOWN_1.
DR NON_TER 1
FT NON_TER 219
SQ SEQUENCE 219 AA; 23944 MW; 7E1B82A14EAF8445 CRC64;

Query Match 83.1%; Score 494.5; DB 2; Length 219;
Best Local Similarity 85.8%; Pred. No. 1.7e-43;
Matches 97; Conservative 7; Mismatches 8; Indels 1; Gaps 1;

QY 1 DVVMTQTPSLPVTGEPASISCRSSQSLVHRNGNTYLHWYLKQPGSKLIHKVSNRF 60
Db 1 ELVMTQPSLSVSLGDAQSISCRSSQSLVHNGNTYLHWYLKQGLSKLIYIVSNRF 60
QY 61 SGVPRFSGSGSGTDTLTKISRVEADLGVYFCQSQSTHVPPLTFGAGTKLEIK 113
Db 61 SGVPRFSGSGSGTDTLTKISRVEADLGVYFCQSQSTHVPG-TFGGGTKLEIK 112

RESULT 3
Q652Q7 PRELIMINARY; PRT; 248 AA.
ID Q652Q7
AC Q652Q7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE B3 (Fv)-PE40 (Fragment).
GN Name=B3 (Fv)-PE40;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92020904; PubMed=1924323;
RA Brinkmann U., Pai L.H., FitzGerald D.J., Willingham M., Pastan I.;
RT "B3(Fv)-PE38KDEL, a single-chain immunotoxin that causes complete
RT regression of a human carcinoma in mice."
RL Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620 (1991).
DR EMBL; S57990; AAB19971.2; -.

Query Match 83.1%; Score 494.5; DB 2; Length 219;
Best Local Similarity 85.8%; Pred. No. 1.7e-43;
Matches 97; Conservative 7; Mismatches 8; Indels 1; Gaps 1;

QY 1 DVVMTQTPSLPVTGEPASISCRSSQSLVHRNGNTYLHWYLKQPGSKLIHKVSNRF 60
Db 1 ELVMTQPSLSVSLGDAQSISCRSSQSLVHNGNTYLHWYLKQGLSKLIYIVSNRF 60
QY 61 SGVPRFSGSGSGTDTLTKISRVEADLGVYFCQSQSTHVPPLTFGAGTKLEIK 113
Db 61 SGVPRFSGSGSGTDTLTKISRVEADLGVYFCQSQSTHVPG-TFGGGTKLEIK 112

RESULT 4
Q6PIH6 PRELIMINARY; PRT; 240 AA.
ID Q6PIH6
AC Q6PIH6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=12477932; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC034142; AAB34142.1; -.
DR HSSP; P01837; 1KB5.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
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DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 240 AA; 26234 MW; 18804D8BB7815C4 CRC64;

Query Match 78.2%; Score 465; DB 2; Length 240;
Best Local Similarity 77.9%; Pred. No. 2.3e-40;
Matches 88; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY 1 DVVMTQTPSLPVTGPEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSKLLIHKVSNRF 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 21 DIVMAQSPSLSVTPGEPASISCRSSQSLHNSGNYFDWYLOKPGQSPQLLIYVGSNRA 80
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SGVPRDFSGSGSGTDTLKLISRVEADLGVPFCSQSTHVPPPLTFGAGTKLELK 113
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 81 SGVPRDFSGSGSGTDTLKLISRVEADVGYYVCMQALQTPPPYFGQGTKEIK 133
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 5
Q9UL80 PRELIMINARY; PRT; 114 AA.
AC Q9UL80;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035034; AAD56270.1; -.
DR PIR; B49002;
DR PIR; S23638; S23638.
DR PIR; S34094; S34094.
DR PIR; S34095; S34095.
DR HSSP; P01625; ILVE.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 114
SQ SEQUENCE 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;

Query Match 78.0%; Score 464; DB 2; Length 114;
Best Local Similarity 77.9%; Pred. No. 1.2e-40;
Matches 88; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

QY 1 DVVMTQTPSLPVTGPEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSKLLIHKVSNRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DVVMTQSPSLPVTLRQPASISCRSSQSPVYSGNTYLNWFQRPQSPRRLIYKVSNRD 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SGVPRDFSGSGSGTDTLKLISRVEADLGVPFCSQSTHVPPPLTFGAGTKLELK 113
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SGVPRDFSGSGSGTDTLKLISRVEADVGYYVCMQGHPPPTFGQGTKEIK 113
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 6
KV2D_HUMAN STANDARD; PRT; 113 AA.
AC P01617;
DT 21-JUL-1986 (Rel. 01, Created)
```

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DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region TEW.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (BENCE-JONES PROTEIN TEW).
RX MEDLINE=74148480; PubMed=4596149;
RA Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
RT "Amino acid sequence of a kappa Bence Jones protein from a case of
   primary amyloidosis.";
RL Biochemistry 12:3763-3780(1973).
RN [2]
RP SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).
RX MEDLINE=73166638; PubMed=4700495;
RA Terry W.D., Page D.L., Kimura S., Isobe T., Osseman E.F.,
RA Glenner G.G.;
RT "Structural identity of Bence Jones and amyloid fibril proteins in a
   patient with plasma cell dyscrasia and amyloidosis.";
RL J. Clin. Invest. 52:1276-1281(1973).
CC -!- MISCELLANEOUS: The major amyloid protein appears to be identical
   with the Bence Jones protein isolated from the same patient.
CC -!- MISCELLANEOUS: This protein was isolated from the urine of a
   patient with plasma cell dyscrasia and amyloidosis.
CC -!- MISCELLANEOUS: The C region of this chain has the INV (1,2)
   marker.
CC PIR; A50370; K2HUTW.
DR HSSP; Q99M37; 1191.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Amyloid; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23
   Framework-1.
FT DOMAIN 24 39
   Complementarity-determining-1.
FT DOMAIN 40 54
   Framework-2.
FT DOMAIN 55 61
   Complementarity-determining-2.
FT DOMAIN 62 93
   Framework-3.
FT DOMAIN 94 102
   Complementarity-determining-3.
FT DOMAIN 103 112
   Framework-4.
FT DISULFID 23 93
   By similarity.
FT NON_TER 113
SQ SEQUENCE 113 AA; 12316 MW; 0C3C30F81F1843CA CRC64;

Query Match 77.9%; Score 463.5; DB 1; Length 113;
Best Local Similarity 77.0%; Pred. No. 1.3e-40;
Matches 87; Conservative 15; Mismatches 10; Indels 1; Gaps 1;

QY 1 DVVMTQTPSLPVTGPEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSKLLIHKVSNRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHNSGDFDYNWYLOKPGQSPZLLIYALSNA 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 SGVPRDFSGSGSGTDTLKLISRVEADLGVPFCSQSTHVPPPLTFGAGTKLELK 113
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SGVPRDFSGSGSGTDTLKLISRVEADVGYYVCMZALQA-PITFGQGTLEIK 112
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 7
Q8TCD0 PRELIMINARY; PRT; 239 AA.
AC Q8TCD0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smillus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022362; AAH22362.1; -
DR PIR; S22658; S22658.
DR PIR; S34095; S34095.
DR PIR; S40324; S40324.
DR PIR; S40374; S40374.
DR PIR; S42267; S42267.
DR PIR; S42268; S42268.
DR HSSP; P01834; 117Z.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_cl.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF07654; CI-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26234 MW; FAGEDC3A3B03871D CRC64;

Query Match 77.7%; Score 462.5; DB 2; Length 239;
Best Local Similarity 78.8%; Pred. No. 4.1e-40;
Matches 89; Conservative 13; Mismatches 10; Indels 1; Gaps 1;

QY 1 DVVMTQPLSLPVTGPGPASISCRSSQSLVHRNGNTYLVHWLQKPGQSPKLLIHKVSNRF 60
DB 21 DVVMTQSPLSFLPVTGPGPASISCRSTQSLVYSDGNTYLVNWFQQRPGQSPRLIYKVSNRD 80
QY 61 SGVPRDFSGSGGTDFTLTKISRVEADLGVFCSQSTHVPPLTFGAGTKLELK 113
DB 81 SGVPRDFSGSGGTDFTLTKISRVEADVGVIYFCMQGTHWPS-TFGQGTLEIK 132

RESULT 8
ID Q6P491 PRELIMINARY; PRT; 239 AA.
AC Q6P491;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smillus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC063599; AAH63599.1; -
DR HSSP; P01837; IKCU.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; CI-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26245 MW; CD7313DDFFD358B3 CRC64;

Query Match 76.6%; Score 455.5; DB 2; Length 239;
Best Local Similarity 75.2%; Pred. No. 2.2e-39;
Matches 85; Conservative 15; Mismatches 12; Indels 1; Gaps 1;

QY 1 DVVMTQPLSLPVTGPGPASISCRSSQSLVHRNGNTYLVHWLQKPGQSPKLLIHKVSNRF 60
DB 21 DVVMTQPLSLPVTGPGPASISCRSSQSLVHRNGNTYLVHWLQKPGQSPRLIYKISNRF 80
QY 61 SGVPRDFSGSGGTDFTLTKISRVEADLGVFCSQSTHVPPLTFGAGTKLELK 113
DB 81 SGVPRDFSGSGGTDFTLTKISRVEADVGVIYFCMQVSHF-PRTFGQGTREIK 132

RESULT 9
KV2E HUMAN
ID KV2E HUMAN STANDARD; PRT; 117 AA.
AC P06309;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region Gm607 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
```

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RN SEQUENCE FROM N.A.
RP MEDLINE=84191506; PubMed=6325927;
RA Klobeck H.G., Solomon A., Zachau H.G.;
RT "Contribution of human V kappa II germ-line genes to light-chain
RT diversity.";
RL Nature 309:73-76(1984).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z00009; -; NOT_ANNOTATED_CDS.
DR PIR; A01889; K2HUGM.
DR HSP; Q99M37; I191.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 4
FT CHAIN 5 117 Ig kappa chain V-II region GM607.
FT DOMAIN 5 27 Framework-1.
FT DOMAIN 28 43 Complementarity-determining-1.
FT DOMAIN 44 58 Framework-2.
FT DOMAIN 59 65 Complementarity-determining-2.
FT DOMAIN 66 97 Framework-3.
FT DOMAIN 98 106 Complementarity-determining-3.
FT DOMAIN 107 116 Framework-4.
FT DISULFID 27 97 By similarity.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;

Query Match 76.2%; Score 453.5; DB 1; Length 117;
Best Local Similarity 77.9%; Pred. No. 1.6e-39;
Matches 88; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 1 DVVMTQPLSLPVTGPEPASISCRSSQSLVHNGNTYLHWYLOKPGQSPKLLIHKVSNR 60
DB 5 DVMTQSPSLPVTGPEPASISCRSSQSLVHNGNTYLHWYLOKPGQSPKLLIHKVSNR 64

QY 61 SGVPRFSGSGGTDTFTLKISRVEAEDLGVYFCQSSTHVPPLTFTGAGTKLEK 113
DB 65 SGVPRFSGSGGTDTFTLKISRVEAEDVGVYCMQGLQTPQ-TFGQGTKEIK 116

RESULT 10
KV2F HUMAN STANDARD; PRT; 133 AA.
AC P06310;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region RPMI 6410 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=86041852; PubMed=2997711;
RA Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and
RT III.";

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RL Nucleic Acids Res. 13:6499-6513(1985).
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z00020; CAA77315.1; -.
DR PIR; A01890; K2HURP.
DR HSP; Q99M37; I191.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 133 Ig kappa chain V-II region RPMI 6410.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 59 Complementarity-determining-1.
FT DOMAIN 60 74 Framework-2.
FT DOMAIN 75 81 Complementarity-determining-2.
FT DOMAIN 82 113 Framework-3.
FT DOMAIN 114 122 Complementarity-determining-3.
FT DOMAIN 123 132 Framework-4.
FT DISULFID 43 113 By similarity.
FT NON_TER 133 133
SQ SEQUENCE 133 AA; 14707 MW; 513CCAF3673009EE CRC64;

Query Match 76.2%; Score 453.5; DB 1; Length 133;
Best Local Similarity 77.9%; Pred. No. 1.8e-39;
Matches 88; Conservative 13; Mismatches 11; Indels 1; Gaps 1;

QY 1 DVVMTQPLSLPVTGPEPASISCRSSQSLVHNGNTYLHWYLOKPGQSPKLLIHKVSNR 60
DB 21 DVMTQSPSLPVTGPEPASISCRSSQSLVHNGNTYLHWYLOKPGQSPKLLIHKVSNR 80

QY 61 SGVPRFSGSGGTDTFTLKISRVEAEDLGVYFCQSSTHVPPLTFTGAGTKLEK 113
DB 81 SGVPRFSGSGGTDTFTLKISRVEAEDVGVYCMQGTW-SWTFQGTKEIK 132

RESULT 11
Q8NEKO
ID Q8NEKO PRELIMINARY; PRT; 239 AA.
AC Q8NEKO;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Hypothetical protein.
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Prostate;
RC MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussid T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 Jones S.J., Marra M.A.,
 "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences,"
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 SEQUENCE FROM N.A.
 TISSUE=Prostate;
 Strauberg R.;
 Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 EMBL; BC030814; AAH30814.1; -
 PIR; S23638; S23638.
 PIR; S34091; S34091.
 PIR; S40342; S40342.
 PIR; S40357; S40357.
 HSSP; P01834; I17Z.
 InterPro; IPR007110; Ig-like.
 InterPro; IPR003597; Ig cl.
 InterPro; IPR003006; Ig_MHC.
 InterPro; IPR003596; Ig_v.
 Pfam; PR07654; Cl-set 1.
 SMART; SM00406; IGV; 1.
 PROSITE; PSS0835; IG_LIKE; 2.
 PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;
 Query Match 76.1%; Score 452.5; DB 2; Length 239;
 Best Local Similarity 76.1%; Pred. No. 4.6e-39;
 Matches 86; Conservative 12; Mismatches 14; Indels 1; Gaps 1;
 QY 1 DVMTQTPLSLPVTGPEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNR 60
 Db 21 DIVMTQPLSLPVTGPEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNR 80
 QY 61 SGVDPFRFSGSGGTDTLTKISRVEADLGVYFCQSQTHVPPLTFGAGTKLELK 113
 Db 81 SGVDPFRFSGSGGTDTLTKISRVEADLGVYFCQSQTHVPPLTFGAGTKLELK 132
 RESULT 12
 KV2A_HUMAN
 ID KV2A_HUMAN STANDARD; PRT; 115 AA.
 AC P01614;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig kappa chain V-II region Cum.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=68242259; PubMed=5586923;
 RA Hilschmann N.;
 RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-
 type).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
 RN [2]
 RP REVISIONS TO 50; 52; 96 AND 97.
 EX MEDLINE=70063440; PubMed=4188189;
 RA Hilschmann N.;
 RT "Molecular basis of antibody formation.";
 RL Naturwissenschaften 56:195-205(1969).
 CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
 -!- MISCELLANEOUS: This is a Bence-Jones protein.

PIR; B91639; K2HUCM.
 DR HSSP; P01751; 1NOB.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; IGV; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 KW Bence-Jones protein; Direct protein sequencing;
 KW Immunoglobulin V region.
 FT DISULFID 24 95
 FT NON_TER 115 115
 SQ SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;
 Query Match 74.6%; Score 444; DB 1; Length 115;
 Best Local Similarity 76.3%; Pred. No. 1.5e-38;
 Matches 87; Conservative 13; Mismatches 12; Indels 2; Gaps 2;
 QY 1 DVMTQTPLSLPVTGPEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNR 59
 Db 2 DIVMTQPLSLPVTGPEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNR 61
 QY 60 FSGVDPFRFSGSGGTDTLTKISRVEADLGVYFCQSQTHVPPLTFGAGTKLELK 113
 Db 62 ASGVDPFRFSGSGGTDTLTKISRVEADLGVYFCQSQTHVPPLTFGAGTKLEIR 114
 RESULT 13
 KV2B_HUMAN
 ID KV2B_HUMAN STANDARD; PRT; 113 AA.
 AC P01615;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig kappa chain V-II region FR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=76253627; PubMed=821524;
 RA Riesen W.F., Jaton J.-C.;
 RT "Variable region sequence of the light chain from a Waldenstroms IgM
 with specificity for phosphorylcholine.";
 RL Biochemistry 15:3829-3833(1976).
 CC -!- MISCELLANEOUS: This chain was isolated from a Waldenstrom's
 macroglobulin that binds phosphorylcholine.
 DR PIR; A01886; K2HUFK.
 DR HSSP; Q99M37; I191.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; IGV; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 39
 FT DOMAIN 40 54
 FT DOMAIN 55 61
 FT DOMAIN 62 93
 FT DOMAIN 94 102
 FT DOMAIN 103 112
 FT DISULFID 23 93
 FT NON_TER 113 113
 SQ SEQUENCE 113 AA; 12660 MW; 0C0DA39E46DB96BE CRC64;
 Query Match 74.0%; Score 440.5; DB 1; Length 113;

Best Local Similarity 75.2%; Pred. No. 3.4e-38;
Matches 85; Conservative 13; Mismatches 14; Indels 1; Gaps 1;

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QY 1 DVVMTOTPLSLPVTGCEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNRF 60
DB 1 DVVMTOSPLFLPVLGEPASIQCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNRF 60
QY 61 SGVDPFRFSGSGGTDFTLKISRVEAEDLGVYFCQSQSTHVPPLTFFGAGTKLELK 113
DB 61 SGVDPFRFSDSGGTDFTLKITRVAEDVGVYCMQATZ-SPYTFGGGTLKLIK 112
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RESULT 14

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KV2C_HUMAN STANDARD; PRT; 112 AA.
ID KV2C_HUMAN
AC P01616;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region MIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
```

SEQUENCE.
RA Dreyer W.J., Gray W.R., Hood L.E.;
RT "The genetic, molecular, and cellular basis of antibody formation:
RT some facts and a unifying hypothesis.";
RL Cold Spring Harb. Symp. Quant. Biol. 32:353-367(1967).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.

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DR PIR; A01887; K2HUML.
DR HSSP; Q99M37; 1191.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
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FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 38 Complementarity-determining-1.
FT DOMAIN 39 53 Framework-2.
FT DOMAIN 54 60 Complementarity-determining-2.
FT DOMAIN 61 92 Complementarity-determining-3.
FT DOMAIN 93 101 Complementarity-determining-4.
FT DOMAIN 102 111 Framework-4.
FT DISULFID 23 92 By similarity.
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12055 MW; E5B22E2FA7ABE481 CRC64;
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Query Match 71.6%; Score 426; DB 1; Length 112;
Best Local Similarity 69.0%; Pred. No. 1.1e-36;
Matches 78; Conservative 21; Mismatches 12; Indels 2; Gaps 2;

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QY 1 DVVMTOTPLSLPVTGCEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNRF 60
DB 1 DIVLTSPLSLPVTGCEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNRF 59
QY 61 SGVDPFRFSGSGGTDFTLKISRVEAEDLGVYFCQSQSTHVPPLTFFGAGTKLELK 113
DB 60 SGVDPFRFSGSGGTDFTLKISRVAZBVGYYCMQALQT-PLTFGGGTNVEIK 111
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RESULT 15

```
KV2F_MOUSE STANDARD; PRT; 113 AA.
ID KV2F_MOUSE
AC P01630;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region 7S34.1.
```

Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE.
RX MEDLINE=83256427; PubMed=6409088;
RA Chang J.-Y., Herbat H., Aebersold R., Braun D.G.;
RT "A new isotype sequence (V kappa 27) of the variable region of kappa-
RT light chains from a mouse hybridoma-derived anti-(streptococcal group
RT A polysaccharide) antibody containing an additional cysteine residue.
RT Application of the dimethylaminobenzene isothiocyanate technique
RT for the isolation of peptides.";
RL Biochem. J. 211:173-180(1983).

CC -!- MISCELLANEOUS: This chain is from a hybridoma-derived monoclonal
CC antibody against the streptococcal group A polysaccharide.
CC PIR; A01913; KMS7S.
DR HSSP; Q99M37; 1191.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Direct protein sequencing; Hybridoma; Immunoglobulin V region;
KW Monoclonal antibody.

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FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 39 Complementarity-determining-1.
FT DOMAIN 40 54 Framework-2.
FT DOMAIN 55 61 Complementarity-determining-2.
FT DOMAIN 62 93 Complementarity-determining-3.
FT DOMAIN 94 102 Complementarity-determining-4.
FT DOMAIN 103 112 Framework-4.
FT DISULFID 23 93 By similarity.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;
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Query Match 70.0%; Score 416.5; DB 1; Length 113;
Best Local Similarity 70.8%; Pred. No. 1.1e-35;
Matches 80; Conservative 14; Mismatches 18; Indels 1; Gaps 1;

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QY 1 DVVMTOTPLSLPVTGCEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNRF 60
DB 1 DIVMTQTAPSLVTPGCEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNRF 60
QY 61 SGVDPFRFSGSGGTDFTLKISRVEAEDLGVYFCQSQSTHVPPLTFFGAGTKLELK 113
DB 61 SGVDPFRFSGSGGTDFTLKISRVEAEDVGVYCMQOREY-PYTFGGGTNVEIK 112
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Search completed: April 18, 2005, 10:03:55
Job time : 85.5 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 10:04:06 ; Search time 70 Seconds
(without alignments)
536.541 Million cell updates/sec

Title: US-10-737-208A-1

Perfect score: 595

Sequence: 1 DVMVTQTPLSLVPTGEPAS.....SOSTHVPPLTFGAGTKLELK 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370683 residues

Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	570	95.8	113	15	US-10-468-370-689
2	570	95.8	113	16	US-10-468-370-689
3	558	93.8	113	15	US-10-468-370-687
4	558	93.8	113	16	US-10-468-370-687
5	547	91.9	114	16	US-10-763-629-18
6	532	89.4	113	15	US-10-468-370-675
7	532	89.4	113	16	US-10-468-370-675
8	530.5	89.2	116	9	US-09-753-436-66
9	530.5	89.2	116	14	US-10-163-942-66
10	529.5	89.0	139	15	US-10-372-481-29
11	529.5	89.0	139	15	US-10-371-797-29
12	526	88.4	113	15	US-10-468-370-685
13	526	88.4	113	16	US-10-468-370-685

Sequence 22, Appl
Sequence 14, Appl
Sequence 35, Appl
Sequence 42, Appl
Sequence 20, Appl
Sequence 47, Appl
Sequence 48, Appl
Sequence 49, Appl
Sequence 683, Appl
Sequence 2014, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 6, Appl
Sequence 681, Appl
Sequence 2012, Appl
Sequence 679, Appl
Sequence 2010, Appl
Sequence 3, Appl
Sequence 27, Appl
Sequence 677, Appl
Sequence 2008, Appl
Sequence 95, Appl
Sequence 2, Appl
Sequence 45, Appl
Sequence 26, Appl
Sequence 2, Appl
Sequence 6, Appl
Sequence 10, Appl
Sequence 85, Appl
Sequence 87, Appl

ALIGNMENTS

RESULT 1
US-10-468-370-689
; Sequence 689, Application US/10468370
; Publication No. US20040082039A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Carr, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Carter, Graham
; APPLICANT: Hamilton, Anita
; APPLICANT: Williams, Stephen
; APPLICANT: Hanlon, Marian
; APPLICANT: Watkins, John
; APPLICANT: Baker, Matthew
; APPLICANT: Way, Jeffrey
; TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-118
; CURRENT APPLICATION NUMBER: US/10/468,370
; PRIOR FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: EP 01103955.9
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: EP 01108291.4
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: PCT/EP02/01690
; NUMBER OF SEQ ID NOS: 689
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 689
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-468-370-689
Query Match 95.8%; Score 570; DB 15; Length 113;
Best Local Similarity 96.5%; Pred. No. 1.6e-45;

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Matches 109; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 DVVMTQPLSLPVTGPSPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNR 60
Db 1 DVVMTQPLSLPVLGQDQASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNR 60
QY 61 SGVPDRFSGSGGTDFTLKISRVEADLGVYFCQSOSTHVPPLTFGAGTKLEK 113
Db 61 SGVPDRFSGSGGTDFTLKISRVEADLGVYFCQSOSTHVPPLTFGAGTKLEK 113

RESULT 2
US-10-468-496-2020
; Sequence 2020, Application US/10468496
; Publication No. US20040180386A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
; TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED
; FILE REFERENCE: IMMUNOGENICITY
; CURRENT APPLICATION NUMBER: US/10/468,496
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR FILING DATE: 2001-03-08
; PRIOR FILING DATE: 2001-03-15
; PRIOR FILING DATE: 2001-03-15
; PRIOR FILING DATE: 2001-03-20
; PRIOR FILING DATE: 2001-03-20
; PRIOR FILING DATE: 2001-03-20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2020
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-496-2020

Query Match 95.8%; Score 570; DB 16; Length 113;
Best Local Similarity 96.5%; Pred. No. 1.6e-45;
Matches 109; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 DVVMTQPLSLPVTGPSPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNR 60
Db 1 DVVMTQPLSLPVLGQDQASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNR 60
QY 61 SGVPDRFSGSGGTDFTLKISRVEADLGVYFCQSOSTHVPPLTFGAGTKLEK 113
Db 61 SGVPDRFSGSGGTDFTLKISRVEADLGVYFCQSOSTHVPPLTFGAGTKLEK 113

RESULT 3
US-10-468-370-687
; Sequence 687, Application US/10468370
; Publication No. US20040082039A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Carr, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Carter, Graham
; APPLICANT: Hamilton, Anita
; APPLICANT: Williams, Stephen
```

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; APPLICANT: Hanlon, Marian
; APPLICANT: Watkins, John
; APPLICANT: Baker, Matthew
; APPLICANT: Way, Jeffrey
; TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-118
; CURRENT APPLICATION NUMBER: US/10/468,370
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: EP 01103955.9
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: EP 01108291.4
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: PCT/EP02/01690
; PRIOR FILING DATE: 2002-02-18
; NUMBER OF SEQ ID NOS: 689
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 687
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-370-687

Query Match 93.8%; Score 558; DB 15; Length 113;
Best Local Similarity 94.7%; Pred. No. 2.1e-44;
Matches 107; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 DVVMTQPLSLPVTGPSPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNR 60
Db 1 DVVMTQPLSLPVLGQDQASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNR 60
QY 61 SGVPDRFSGSGGTDFTLKISRVEADLGVYFCQSOSTHVPPLTFGAGTKLEK 113
Db 61 SGVPDRFSGSGGTDFTLKISRVEADLGVYFCQSOSTHVPPLTFGAGTKLEK 113

RESULT 4
US-10-468-496-2018
; Sequence 2018, Application US/10468496
; Publication No. US20040180386A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
; TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED
; FILE REFERENCE: IMMUNOGENICITY
; CURRENT APPLICATION NUMBER: US/10/468,496
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: 01105777.5
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 01106538.0
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01106536.4
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01107012.5
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 01106899.6
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 2036
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2018
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: MHC class II binding epitope
US-10-468-496-2018

Query Match          93.8%; Score 558; DB 16; Length 113;
Best Local Similarity 94.7%; Pred. No. 2.1e-44;
Matches 107; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DVVMTQTPLSLPVTGPEPASISCRSSQSLVHRNGNTYLHWYLPKQSPKLLIHKVSNRF 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DVVMTQTGSLPVSAGDQASISCRSSQSLVHRNGNTYLHWYLPKQSPKLLIHKVSNRF 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SGVPDRFSGSGSDTFTLKISRVEADLGVYFCQSQTTHVPPLTFGAGTKLEIK 113
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 SGVPDRFSGSGSDTFTLKISRVEADLGVYFCQSQTTHVPPLTFGAGTKLEIK 113
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
US-10-762-629-18
; Sequence 18, Application US/10762629
; Publication No. US20040141964A1
; GENERAL INFORMATION:
; APPLICANT: Abdel-Meguid, Sherin
; APPLICANT: Ho, Yen Sen
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Taylor, Alexander H.
; TITLE OF INVENTION: Recombinant IL-18 Antagonists Useful in
; TITLE OF INVENTION: Treatment of IL-18 Mediated Disorders
; FILE REFERENCE: P50897
; CURRENT APPLICATION NUMBER: US/10/762,629
; CURRENT FILING DATE: 2004-01-22
; PRIOR APPLICATION NUMBER: US/09/914,695
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: PCT/US00/07349
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/125,299
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-762-629-18

Query Match          91.9%; Score 547; DB 16; Length 114;
Best Local Similarity 92.0%; Pred. No. 2.3e-43;
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DVVMTQTPLSLPVTGPEPASISCRSSQSLVHRNGNTYLHWYLPKQSPKLLIHKVSNRF 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DVVMTQTPLSLPVSAGDQASISCRSSQSLVHRNGNTYLHWYLPKQSPKLLIHKVSNRF 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SGVPDRFSGSGSDTFTLKISRVEADLGVYFCQSQTTHVPPLTFGAGTKLEIK 113
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 SGVPDRFSGSGSDTFTLKISRVEADLGVYFCQSQTTHVPPLTFGAGTKLEIK 113
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RESULT 6
US-10-468-370-675
; Sequence 675, Application US/10468370
; Publication No. US20040082039A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Carr, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Carter, Graham
; APPLICANT: Hamilton, Anita
; APPLICANT: Williams, Stephen
; APPLICANT: Hanlon, Marian
; APPLICANT: Watkins, John
; APPLICANT: Baker, Matthew
; APPLICANT: Way, Jeffrey
; TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED

; OTHER INFORMATION: MHC class II binding epitope
US-10-468-496-2006

Query Match          89.4%; Score 532; DB 15; Length 113;
Best Local Similarity 89.4%; Pred. No. 5.6e-42;
Matches 101; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 DVVMTQTPLSLPVTGPEPASISCRSSQSLVHRNGNTYLHWYLPKQSPKLLIHKVSNRF 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DVVMTQSPGTLFVSLGERATISCRSSQSLVHRNGNTYLHWYLPKQSPKLLIHKVSNRF 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SGVPDRFSGSGSDTFTLKISRVEADLGVYFCQSQTTHVPPLTFGAGTKLEIK 113
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 SGVPDRFSGSGSDTFTLTISRLEADLAVYFCQSQTTHVPPLTFGAGTKLEIK 113
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
US-10-468-496-2006
; Sequence 2006, Application US/10468496
; Publication No. US20040180386A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
; TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED
; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-117
; CURRENT APPLICATION NUMBER: US/10/468,496
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: 01105777.5
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 01106538.0
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01106536.4
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01107012.5
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 01106899.6
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 2036
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2006
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-496-2006

Query Match          89.4%; Score 532; DB 16; Length 113;
Best Local Similarity 89.4%; Pred. No. 5.6e-42;
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;
; SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-10-163-942-66

Query Match      89.2%; Score 530.5; DB 14; Length 116;
Best Local Similarity 88.5%; Pred. No. 7.9e-42;
Matches 100; Conservative 9; Mismatches 3; Indels 1; Gaps 1;

QY 1 DVVMTQTPSLPVTGEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNRF 60
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 5 DVMTQSPSLPVTGEPASISCRSSQSLVHNSGDTYLLHWYLOKPGQSPQLLIYKVSNR 64
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 SGVPDRFSGSGGTDFTLKISRVEAEDLGVYFCQSQTTHVPLTFGAGTKLELK 113
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 65 SGVPDRFSGSGGTDFTLKISRVEAEDGVYVYCSQSTHV-PYTFGGGTVKEIK 116
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 10
US-10-372-481-29
; Sequence 29, Application US/10372481
; Publication No. US20030202975A1
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F.
; TITLE OF INVENTION: REAGENTS AND TREATMENT METHODS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 5405.306
; CURRENT APPLICATION NUMBER: US/10/372,481
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: PCT/US03/05549
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 60/420,472
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/359,419
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-372-481-29

Query Match      89.0%; Score 529.5; DB 15; Length 139;
Best Local Similarity 91.2%; Pred. No. 1.2e-41;
Matches 103; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 1 DVVMTQTPSLPVTGEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNRF 60
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 5 DVMTQSPSLPVTGEPASISCRSSQSLVHNSGDTYLLHWYLOKPGQSPQLLIYKVSNR 64
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 SGVPDRFSGSGGTDFTLKISRVEAEDLGVYFCQSQTTHVPLTFGAGTKLELK 113
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 65 SGVPDRFSGSGGTDFTLKISRVEAEDGVYVYCSQSTHV-PYTFGGGTVKEIK 116
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 11
US-10-371-797-29
; Sequence 29, Application US/10371797
; Publication No. US20040001828A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: TUSCANO, Joseph
; APPLICANT: TEDDER, Thomas
; TITLE OF INVENTION: TREATMENT METHODS USING ANTI-CD22
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 39754-0951
; CURRENT APPLICATION NUMBER: US/10/371,797
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 60/420,472
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/359,419
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29

; LENGTH: 139
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-371-797-29

Query Match      89.0%; Score 529.5; DB 15; Length 139;
Best Local Similarity 91.2%; Pred. No. 1.2e-41;
Matches 103; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 1 DVVMTQTPSLPVTGEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNRF 60
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 20 DVMTQTPSLPVLGDAQASISCRSSQSLVHNSGNTYLHWYLOKPGQSPKLLIYKVSNR 79
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 SGVPDRFSGSGGTDFTLKISRVEAEDLGVYFCQSQTTHVPLTFGAGTKLELK 113
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 80 SGVPDRFSGSGGTDFTLKISRVEAEDLGVYFCQSQSTHV-PYTFGGGTVKEIK 131
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 12
US-10-468-370-685
; Sequence 685, Application US/10468370
; Publication No. US20040082039A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Carr, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Carter, Graham
; APPLICANT: Hamilton, Anita
; APPLICANT: Williams, Stephen
; APPLICANT: Hanlon, Marian
; APPLICANT: Watkins, John
; APPLICANT: Baker, Matthew
; APPLICANT: Way, Jeffrey
; TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-118
; CURRENT APPLICATION NUMBER: US/10/468,370
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: EP 01103955.9
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: EP 01108291.4
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: PCT/EP02/01690
; PRIOR FILING DATE: 2002-02-18
; NUMBER OF SEQ ID NOS: 689
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 685
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: De-immunized MHC class II binding epitope
US-10-468-370-685

Query Match      88.4%; Score 526; DB 15; Length 113;
Best Local Similarity 86.7%; Pred. No. 2e-41;
Matches 98; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 1 DVVMTQTPSLPVTGEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNRF 60
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 DVMTQSPGTTLPVSLGERATISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIYKVSNR 60
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 SGVPDRFSGSGGTDFTLKISRVEAEDLGVYFCQSQTTHVPLTFGAGTKLELK 113
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 SGVPDRFSGSGGTDFTLTISRLEADMAVYFCQSQTTHVPLTFGGGTVKEIK 113
   :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 13
US-10-468-496-2016
; Sequence 2016, Application US/10468496
; Publication No. US20040180386A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
```

```
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
; TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED
; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-117
; CURRENT APPLICATION NUMBER: US/10/468,496
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: 01105777.5
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 01106538.0
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01106536.4
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01107012.5
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 01106899.6
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 2036
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2016
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-496-2016

Query Match      88.4%; Score 526; DB 16; Length 113;
Best Local Similarity 86.7%; Pred. No. 2e-41;
Matches 98; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 1 DVVMTQTPSLPVTGPGEPAISCRSSQSLVHRNGNTYHLHWYLOKPGQSPKLLIHKVSNRF 60
Db 1 DVVMTQTPSLPVTGPGEPAISCRSSQSLVHRNGNTYHLHWYLOKPGQSPKLLIHKVSNRF 60
QY 61 SGVDPDRFSGSGGTDFTLKISRVEAEDLGVYFCQSOSTHVPPLTFGAGTKLEIK 113
Db 61 SGVDPDRFSGSGGTDFTLKISRLEAEDMAVYFCQSOSTHVPPLTFGGGKVEIK 113

RESULT 14
US-10-741-657A-22
; Sequence 22, Application US/10741657A
; Publication No. US20040197325A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs
; TITLE OF INVENTION: ANTIBODIES AGAINST GPR64 AND USES THEREOF
; FILE REFERENCE: 05882.0177.NPUS01
; CURRENT APPLICATION NUMBER: US/10/741,657A
; CURRENT FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 22
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-741-657A-22

Query Match      88.3%; Score 525.5; DB 16; Length 112;
Best Local Similarity 90.3%; Pred. No. 2.2e-41;
Matches 102; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 1 DVVMTQTPSLPVTGPGEPAISCRSSQSLVHRNGNTYHLHWYLOKPGQSPKLLIHKVSNRF 60
Db 1 DVVMTQTPSLPVTGPGEPAISCRSSQSLVHRNGNTYHLHWYLOKPGQSPKLLIHKVSNRF 60
QY 61 SGVDPDRFSGSGGTDFTLKISRVEAEDLGVYFCQSOSTHVPPLTFGAGTKLEIK 113
Db 61 SGVDPDRFSGSGGTDFTLKISRVEAEDLGVYFCQSOSTHVPPLTFGAGTKLEIK 113

RESULT 15
US-10-741-657A-14
; Sequence 14, Application US/10741657A
; Publication No. US20040197325A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs
; TITLE OF INVENTION: ANTIBODIES AGAINST GPR64 AND USES THEREOF
; FILE REFERENCE: 05882.0177.NPUS01
; CURRENT APPLICATION NUMBER: US/10/741,657A
; CURRENT FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-741-657A-14

Query Match      88.0%; Score 523.5; DB 16; Length 112;
Best Local Similarity 90.3%; Pred. No. 3.4e-41;
Matches 102; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY 1 DVVMTQTPSLPVTGPGEPAISCRSSQSLVHRNGNTYHLHWYLOKPGQSPKLLIHKVSNRF 60
Db 1 DVVMTQTPSLPVTGPGEPAISCRSSQSLVHRNGNTYHLHWYLOKPGQSPKLLIHKVSNRF 60
QY 61 SGVDPDRFSGSGGTDFTLKISRVEAEDLGVYFCQSOSTHVPPLTFGAGTKLEIK 113
Db 61 SGVDPDRFSGSGGTDFTLKISRVEAEDLGVYFCQSOSTHVPPLTFGAGTKLEIK 113

Search completed: April 18, 2005, 10:17:26
Job time : 71 secs
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OM protein - protein search, using sw model

Run on: April 18, 2005, 09:57:36 ; Search time 19 seconds
(without alignments)
443.965 Million cell updates/sec

Title: US-10-737-208A-1
Perfect score: 595
Sequence: 1 DVVMTQTPLSLVPTGEPAS.....SQSTHVPPLTFGAGTKLEIK 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/iaa/5A_COMB.pep:**
- 2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:**
- 3: /cgn2_6/prodata/1/iaa/6A_COMB.pep:**
- 4: /cgn2_6/prodata/1/iaa/6B_COMB.pep:**
- 5: /cgn2_6/prodata/1/iaa/PCUS_COMB.pep:**
- 6: /cgn2_6/prodata/1/iaa/backfiles1.pep:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	547	91.9	114	4	US-09-914-695-18
2	533.5	89.7	113	4	US-09-232-290-4
3	530.5	89.2	116	1	US-08-482-882-66
4	530.5	89.2	116	2	US-08-483-389-66
5	530.5	89.2	116	2	US-08-487-113D-66
6	530.5	89.2	116	2	US-08-473-503-66
7	530.5	89.2	116	2	US-08-483-932-66
8	530.5	89.2	116	2	US-08-720-420A-66
9	530.5	89.2	116	3	US-08-714-017-66
10	530.5	89.2	116	3	US-08-475-680-66
11	530.5	89.2	131	3	US-08-589-939-7
12	526.5	88.5	638	3	US-09-070-637-20
13	526	88.4	218	5	PCT-US94-14106-61
14	523.5	88.0	131	1	US-08-398-613A-48
15	523.5	88.0	131	1	US-08-398-612A-48
16	523.5	88.0	131	1	US-08-398-611A-48
17	523.5	88.0	131	2	US-08-491-334A-48
18	523.5	88.0	131	3	US-09-027-449-35
19	523.5	88.0	131	3	US-08-804-444A-35
20	523.5	88.0	131	3	US-09-026-985-35
21	523.5	88.0	131	4	US-09-121-952A-35
22	523.5	88.0	131	4	US-09-234-340A-35
23	523.5	88.0	242	1	US-08-398-613A-56
24	523.5	88.0	242	1	US-08-398-612A-56
25	523.5	88.0	242	1	US-08-398-611A-56
26	523.5	88.0	242	1	US-08-491-334A-56
27	523.5	88.0	242	3	US-09-027-449-42

28	523.5	88.0	242	3	US-08-804-444A-42	Sequence 42, Appl
29	523.5	88.0	242	3	US-09-026-985-42	Sequence 42, Appl
30	523.5	88.0	242	4	US-09-121-952A-42	Sequence 42, Appl
31	523.5	88.0	242	4	US-09-234-340A-42	Sequence 42, Appl
32	518.5	87.1	112	4	US-09-518-737-4	Sequence 4, Appl
33	518.5	87.1	246	1	US-08-257-341-7	Sequence 7, Appl
34	518.5	87.1	252	1	US-08-133-804-4	Sequence 4, Appl
35	518.5	87.1	252	1	US-08-461-838-4	Sequence 4, Appl
36	518.5	87.1	252	2	US-08-461-386-4	Sequence 4, Appl
37	518.5	87.1	367	2	US-08-257-341-5	Sequence 5, Appl
38	517.5	87.0	238	2	US-08-224-591-12	Sequence 12, Appl
39	517.5	87.0	238	2	US-08-392-338A-21	Sequence 21, Appl
40	517.5	87.0	238	2	US-08-926-789-12	Sequence 12, Appl
41	517.5	87.0	238	3	US-09-166-750-21	Sequence 21, Appl
42	517.5	87.0	238	3	US-09-166-093-21	Sequence 21, Appl
43	517.5	87.0	238	3	US-09-172-019-21	Sequence 21, Appl
44	517.5	87.0	238	3	US-09-166-094-21	Sequence 21, Appl
45	517.5	87.0	238	4	US-09-443-213-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-09-914-695-18
; Sequence 18, Application US/09914695
; Patent No. 6706487
; GENERAL INFORMATION:
; APPLICANT: Abdel-Meguid, Sherin
; APPLICANT: Ho, Yen Sen
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Taylor, Alexander H.
; TITLE OF INVENTION: Recombinant IL-18 Antagonists Useful in
; TITLE OF INVENTION: Treatment of IL-18 Mediated Disorders
; FILE REFERENCE: P50897
; CURRENT APPLICATION NUMBER: US/09/914,695
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: PCT/US00/07349
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/125,299
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-914-695-18
Query Match 91.9%; Score 547; DB 4; Length 114;
Best Local Similarity 92.0%; Pred. No. 7, 4e-46;
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 1 DVVMTQTPLSLVPTGEPASISCRSSQLVHRNGNTYHLWYLOKFGQSPKLIHKVSNRF 60
Db 1 DVVMTQTPLSLVPTGEPASISCRSSQLVHRNGNTYHLWYLOKFGQSPKLIHKVSNRF 60
QY 61 SGVPRFSGSGGTDTLTKISRVEADLGVPFCQSOSTHVPPLTFGAGTKLEIK 113
Db 61 SGVPRFSGSGGTDTLTKISRVEADLGVPFCQSOSTHVPPLTFGAGTKLEIK 113
RESULT 2
US-09-232-290-4
; Sequence 4, Application US/09232290A
; Patent No. 6815540
; GENERAL INFORMATION:
; APPLICANT: PLUCKTHUN, ANDREAS
; APPLICANT: NIEBA, LARS
; APPLICANT: HONEGER, ANNEMARIE
; TITLE OF INVENTION: IMMUNOGLOBULIN SUPER FAMILY DOMAINS AND FRAGMENTS WITH
; TITLE OF INVENTION: INCREASED SOLUBILITY
; FILE REFERENCE: MORPHO/7

LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-389-66

Query Match 89.2%; Score 530.5; DB 2; Length 116;
Best Local Similarity 88.5%; Pred. No. 3e-44;
Matches 100; Conservative 9; Mismatches 3; Indels 1; Gaps 1;

QY 1 DVVMTQTLPLSLPVTGEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLIHKVSNRF 60
DB 5 DIVMTQSLSLPVTGEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPQLLIYKVSNNRF 64
QY 61 SGVPRFSGSGSGTDTFLKISRVEADLGVYFCQSQSTHVPPLTFGAGTKLELK 113
DB 65 SGVPRFSGSGSGTDTFLKISRVEADLGVYVCQSSTHV-PYTFQGQTKVEIK 116

RESULT 5

US-08-487-113D-66
Sequence 66, Application US/08487113D
Patent No. 5837822
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,113D
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,754
FILING DATE: 05-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5837822and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32744
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-487-113D-66

Query Match 89.2%; Score 530.5; DB 2; Length 116;
Best Local Similarity 88.5%; Pred. No. 3e-44;
Matches 100; Conservative 9; Mismatches 3; Indels 1; Gaps 1;

QY 1 DVVMTQTLPLSLPVTGEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLIHKVSNRF 60
DB 5 DIVMTQSLSLPVTGEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPQLLIYKVSNNRF 64
QY 61 SGVPRFSGSGSGTDTFLKISRVEADLGVYFCQSQSTHVPPLTFGAGTKLELK 113
DB 65 SGVPRFSGSGSGTDTFLKISRVEADLGVYVCQSSTHV-PYTFQGQTKVEIK 116

RESULT 6

US-08-473-503-66
Sequence 66, Application US/08473503
Patent No. 5869262
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,503
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286,754
FILING DATE: 05-AUG-1994
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5869262and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32178
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-720-420A-66

Query Match 89.2%; Score 530.5; DB 2; Length 116;
Best Local Similarity 88.5%; Pred. No. 3e-44;
Matches 100; Conservative 9; Mismatches 3; Indels 1; Gaps 1;
QY 1 DVVMTQPLSLPVTGPEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNRF 60
Db 5 DIVMTQSPSLPVTGPEPASISCRSSQSLVHSGDYLHWYLOKPGQSPQLLIYKVS 64
QY 61 SGVPRFSGSGSGTDTLKLISRVEADLGVYFCSTHVPPLTFGAGTKLELK 113
Db 65 SGVPRFSGSGSGTDTLKLISRVEADVGVIYCSQSTHV-PYTFGGQTKVEIK 116

RESULT 9

US-08-714-017-66
Sequence 66, Application US/08714017
Patent No. 6040176
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,017
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286,754
FILING DATE:
FILING DATE: 05-AUG-1993
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 05-JUN-1992
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6040176and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32178
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-714-017-66

Query Match 89.2%; Score 530.5; DB 3; Length 116;
Best Local Similarity 88.5%; Pred. No. 3e-44;
Matches 100; Conservative 9; Mismatches 3; Indels 1; Gaps 1;
QY 1 DVVMTQPLSLPVTGPEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNRF 60
Db 5 DIVMTQSPSLPVTGPEPASISCRSSQSLVHSGDYLHWYLOKPGQSPQLLIYKVS 64
QY 61 SGVPRFSGSGSGTDTLKLISRVEADLGVYFCSTHVPPLTFGAGTKLELK 113
Db 65 SGVPRFSGSGSGTDTLKLISRVEADVGVIYCSQSTHV-PYTFGGQTKVEIK 116

RESULT 10

US-08-475-680-66
Sequence 66, Application US/08475680
Patent No. 6100383
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,680
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286,754
FILING DATE: 05-AUG-1994
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6100383and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32178
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-475-680-66

Query Match

89.2%; Score 530.5; DB 3; Length 116;

Best Local Similarity 88.5%; Pred. No. 3e-44; Mismatches 9; Indels 1; Gaps 1;
Matches 100; Conservative

QY 1 DVVMTQTPSLPVTGPEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNRF 60
Db 5 DIVMTQSPSLPVTGPEPASISCRSSQSLVHNSGNTYLHWYLOKPGQSPKLLIYKVSNR 64
QY 61 SGVPDRFSGSGGTDFTLKISRVEAEDLGVYFCQSSTHVPPLTFGAGTKLEK 113
Db 65 SGVPDRFSGSGGTDFTLKISRVEAEDLGVYFCQSSTHVPPLTFGAGTKLEK 116

RESULT 11

US-08-589-939-7
Sequence 7, Application US/08589939
Patent No. 6015662

GENERAL INFORMATION:

APPLICANT: Hackett, Jr., John R.
APPLICANT: Hoff, Jane A.
APPLICANT: Ostrow, David H.
APPLICANT: Golden, Alan M.
TITLE OF INVENTION: REAGENTS FOR USE AS CALIBRATORS AND
TITLE OF INVENTION: CONTROLS
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: US
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/589,939
FILING DATE:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 5865.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-935-1729
TELEFAX: 847-938-2623
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-589-939-7

Query Match 89.2%; Score 530.5; DB 3; Length 131;
Best Local Similarity 91.2%; Pred. No. 3.4e-44;
Matches 103; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 1 DVVMTQTPSLPVTGPEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNRF 60
Db 20 DVVMTQTPSLPVTGPEPASISCRSSQSLVHNSGNTYLHWYLOKPGQSPKLLIYKVSNR 79
QY 61 SGVPDRFSGSGGTDFTLKISRVEAEDLGVYFCQSSTHVPPLTFGAGTKLEK 113
Db 80 SGVPDRFSGSGGTDFTLKISRVEAEDLGVYFCQSSTHVPPLTFGAGTKLEK 131

RESULT 12

US-09-070-637-20
Sequence 20, Application US/09070637A
Patent No. 6132722

GENERAL INFORMATION:

APPLICANT: SIEMERS, NATHAN O.
APPLICANT: YARNOLD, SUSAN
APPLICANT: SENTER, PETER D.

TITLE OF INVENTION: RECOMBINANT ANTIBODY-ENZYME FUSION PROTEINS

FILE REFERENCE: 9197P-83-1

CURRENT APPLICATION NUMBER: US/09/070,637A

CURRENT FILING DATE: 1998-04-30

EARLIER APPLICATION NUMBER: 60/045,888

EARLIER FILING DATE: 1997-05-07

NUMBER OF SEQ ID NOS: 21

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 20

LENGTH: 638

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Amino acid

OTHER INFORMATION: sequence for L49-sfv-bl including PelB leader

US-09-070-637-20

Query Match 88.5%; Score 526.5; DB 3; Length 638;
Best Local Similarity 89.4%; Pred. No. 4.5e-43;
Matches 101; Conservative 6; Mismatches 5; Indels 1; Gaps 1;

QY 1 DVVMTQTPSLPVTGPEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNRF 60
Db 160 DFVMTQTPSLPVTGPEPASISCRSSQSLVHNSGNTYLHWYLOKPGQSPKLLIYKVSNR 219

QY 61 SGVPDRFSGSGGTDFTLKISRVEAEDLGVYFCQSSTHVPPLTFGAGTKLEK 113

Db 220 SGVPDRFSGSGGTDFTLKISRVEAEDLGVYFCQSSTHVPPLTFGAGTKLEK 271

RESULT 13

PCT-US94-14106-61

Sequence 61, Application PC/TUS9414106

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Process for Generating Specific Antibodies

NUMBER OF SEQUENCES: 61

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII (text)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/14106

FILING DATE:

CLASSIFICATION:

INFORMATION FOR SEQ ID NO: 61:

SEQUENCE CHARACTERISTICS:

LENGTH: 218 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US94-14106-61

Query Match 88.4%; Score 526; DB 5; Length 218;

Best Local Similarity 92.0%; Pred. No. 1.6e-43;

Matches 104; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

QY 1 DVVMTQTPSLPVTGPEPASISCRSSQSLVHRNGNTYLHWYLOKPGQSPKLLIHKVSNRF 60

Db 1 DVVMTQTPSLPVTGPEPASISCRSSQSLVHNSGNTYLHWYLOKPGQSPKLLIYKVSNR 60

QY 61 SGVPDRFSGSGGTDFTLKISRVEAEDLGVYFCQSSTHVPPLTFGAGTKLEK 113

Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDLGVYFCQSSTHVPPLTFGAGTKLEK 111

RESULT 14

US-08-398-613A-48

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 09:41:10 ; Search time 62 Seconds
(without alignments)
704,902 Million cell updates/sec

Title: US-10-737-208A-2
Perfect score: 593
Sequence: 1 EVQLVQSGAEVEKPGASVKI.....YYCVSGMEYWGQGTSTVTVSS 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	593	100.0	113	8 ADP42957	Adp42957 Humanised
2	593	100.0	575	8 ADP42961	Adp42961 Humanised
3	561	94.6	113	5 AAE27853	Aae27853 Mouse 14.
4	561	94.6	113	5 ADG57525	Adg57525 14.18 ant
5	556	93.8	113	5 AAE27855	Aae27855 Mouse 14.
6	556	93.8	113	5 ADG67527	Adg67527 14.18 ant
7	556	93.8	153	2 AAE11597	Aae11597 Murine mo
8	536	90.4	113	5 AAE27851	Aae27851 Mouse 14.
9	536	90.4	113	5 ADG67523	Adg67523 14.18 ant
10	527	88.9	113	5 AAE27841	Aae27841 Mouse 14.
11	527	88.9	113	5 ADG67513	Adg67513 14.18 ant
12	524	88.4	113	5 AAE27849	Aae27849 Mouse 14.
13	524	88.4	113	5 ADG67521	Adg67521 14.18 ant
14	521	87.9	113	5 AAE27843	Aae27843 Mouse 14.
15	521	87.9	113	5 ADG67515	Adg67515 14.18 ant
16	520	87.7	113	5 AAE27847	Aae27847 Mouse 14.
17	520	87.7	113	5 ADG67519	Adg67519 14.18 ant
18	514	86.7	113	5 AAE27845	Aae27845 Mouse 14.
19	514	86.7	113	5 ADG67517	Adg67517 14.18 ant
20	493.5	83.2	259	5 ABG31023	Abg31023 Mouse sin
21	493.5	83.2	259	7 ADD25452	Add25452 Binding d
22	493.5	83.2	259	7 ADM42727	Adm42727 Synthetic
23	483.5	81.5	176	8 ADO43522	Ado43522 Amino aci
24	479.5	80.9	467	6 AAE38408	Aae38408 Mouse vir
25	473.5	79.8	120	2 AAR59985	Aar59985 U7.6 heav

26	473.5	79.8	120	2 AAR88752	Aar88752 scFv U7.6
27	473.5	79.8	152	8 ADJ57084	Adj57084 3G4 antib
28	473.5	79.8	159	8 ADJ57088	Adj57088 3G4-28VH-
29	468.5	79.0	120	2 AAR88754	Aar88754 scFv U7.6
30	467.5	78.8	263	2 AAW90226	Aaw90226 Anti-B7.2
31	467.5	78.8	268	2 AAW90222	Aaw90222 Anti-B7.2
32	467.5	78.8	580	2 AAW90217	Aaw90217 Bispecific
33	464	78.2	130	5 AAU70768	Aau70768 Hepatitis
34	464	78.2	130	7 ADC85022	Adc85022 HBV HBCAg
35	464	78.2	130	8 ADK14579	Adk14579 Hepatitis
36	463.5	78.2	276	2 AAW90227	Aaw90227 Anti-B7.1
37	463.5	78.2	281	2 AAW90223	Aaw90223 Anti-B7.1
38	461.5	77.8	556	2 AAW90218	Aaw90218 Bispecific
39	458	77.2	267	3 AAB09776	Aab09776 TMV 30K m
40	455	76.7	119	8 ADR73598	Adr73598 Humanised
41	455	76.7	138	8 ADR73603	Adr73603 HuPAR34.8
42	453	76.4	136	2 AAW06442	Aaw06442 HUMC3 VH
43	452.5	76.3	214	6 ABP96756	Abp96756 TSH recep
44	452.5	76.3	214	6 ABP96755	Abp96755 TSH recep
45	452	76.2	117	2 AAW84097	Aaw84097 Humanised

ALIGNMENTS

RESULT 1
ID: ADP42957 standard; protein; 113 AA.
XX AC ADP42957;
XX DT 23-SEP-2004 (first entry)
XX DE Humanised immunoglobulin heavy chain variable region SEQ ID NO:2.
XX KW immunoglobulin; variable region; antibody; GD2; cytostatic; gene therapy;
XX KW cancer; cell surface glycosphingolipid.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Region 1. .25
FT /label= huVHFR1
FT /note= "framework region 1"
FT Region 36. .49
FT /label= huVHFR2
FT /note= "framework region 2"
FT Region 67. .98
FT /label= huVHFR3
FT /note= "framework region 3"
FT Region 103. .113
FT /label= huVHFR4
FT /note= "framework region 4"
XX WO2004055056-A1.
XX 01-JUL-2004.
XX 16-DEC-2003; 2003WO-EP014295.
XX 17-DEC-2002; 2002US-0433945P.
XX (MERE) MERCK PATENT GMBH.
XX Gillies SD, Lo K;
XX WPI; 2004-488049/46.
XX New modified m4.18 antibodies with reduced immunogenicity and that
XX specifically bind the human cell surface glycosphingolipid GD2, useful
XX for treating cancer.
XX Claim 2; SEQ ID NO: 2; 51pp; English.

XX The invention relates to a novel antibody variable region, where the
CC antibody variable region specifically binds to human cell surface
CC glycosphingolipid GD2. An antibody variable region of the invention has
CC cytostatic activity, and may have a use in gene therapy. The antibody may
CC be used for treating cancer. The nucleic acid or cell is useful for
CC manufacturing a medicament that may be used for treating diseases such as
CC cancer. The present sequence represents humanised immunoglobulin heavy
CC chain variable region.
XX
SQ Sequence 113 AA;

Query Match 100.0%; Score 593; DB 8; Length 113;
Best Local Similarity 100.0%; Pred. No. 2e-45; Indels 0; Gaps 0;
Matches 113; Conservative 0; Mismatches 0;
QY 1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNNMWRQNIKSLWIGAIDPYYGTSY 60
Db 1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNNMWRQNIKSLWIGAIDPYYGTSY 60
QY 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDATVYVCVSGMEYWGQTSVTSS 113
Db 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDATVYVCVSGMEYWGQTSVTSS 113

RESULT 2
ADP42961
ID ADP42961 standard; protein; 575 AA.
XX
AC ADP42961;
XX
XX
DT 23-SEP-2004 (first entry)
XX
DE Humanised immunoglobulin heavy chain-IL-2 fusion protein SEQ ID NO:6.
XX immunoglobulin; variable region; antibody; GD2; cytostatic; gene therapy;
KW cancer; cell surface glycosphingolipid; IL-2.
XX
OS Synthetic.
XX
XX WO2004055056-A1.
PN
PD 01-JUL-2004.
XX
XX 16-DEC-2003; 2003WO-BP014295.
XX
XX 17-DEC-2002; 2002US-0433945P.
XX
XX (MERE) MERCK PATENT GMBH.
XX
XX Gillies SD, Lo K;
XX
XX WPI; 2004-488049/46.
DR N-PSDB; ADP42959.
XX
XX New modified m14.18 antibodies with reduced immunogenicity and that
PT specifically bind the human cell surface glycosphingolipid GD2, useful
PT for treating cancer.
XX
XX Disclosure; SEQ ID NO 6; 51pp; English.
XX
XX The invention relates to a novel antibody variable region, where the
CC antibody variable region specifically binds to human cell surface
CC glycosphingolipid GD2. An antibody variable region of the invention has
CC cytostatic activity, and may have a use in gene therapy. The antibody may
CC be used for treating cancer. The nucleic acid or cell is useful for
CC manufacturing a medicament that may be used for treating diseases such as
CC cancer. The present sequence represents an immunoglobulin heavy chain-IL-
CC 2 fusion protein.
XX
SQ Sequence 575 AA;

Query Match 100.0%; Score 593; DB 8; Length 575;

Best Local Similarity 100.0%; Pred. No. 1.1e-44; Indels 0; Gaps 0;
Matches 113; Conservative 0; Mismatches 0;
QY 1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNNMWRQNIKSLWIGAIDPYYGTSY 60
Db 1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNNMWRQNIKSLWIGAIDPYYGTSY 60
QY 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDATVYVCVSGMEYWGQTSVTSS 113
Db 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDATVYVCVSGMEYWGQTSVTSS 113

RESULT 3
AAE27853
ID AAE27853 standard; protein; 113 AA.

XX
AC AAE27853;
XX
DT 13-DEC-2002 (first entry)
XX
DE Mouse 14.18 antibody VH region #1.
XX
KW Mouse; fusion protein; immunological; major histocompatibility complex;
KW MHC; gastric upset; nausea; 14.18 antibody.
XX
OS Mus sp.

XX
XX WO200266514-A2.
XX
XX 29-AUG-2002.

XX
XX 18-FEB-2002; 2002WO-EP001690.
XX
XX 19-FEB-2001; 2001EP-00103955.
PR 05-APR-2001; 2001EP-00108291.

XX
XX (MERE) MERCK PATENT GMBH.
XX
XX Gillies S, Carr FJ, Jones T, Carter G, Hamilton A, Williams S;
PI Hanlon M, Watkins J, Baker M, Way JC;
XX
XX WPI; 2002-667054/71.

XX
XX New modified fusion protein with reduced immunogenicity, useful for
PT combining favorable properties of a composition, comprises an
PT immunoglobulin molecule linked to a non-immunoglobulin target
PT polypeptide.
XX
XX Example 19; Page 78; 92pp; English.

XX
XX The invention relates to an immunogenically modified fusion protein
CC derived from a parent fusion protein, comprising first and second
CC proteins/polypeptides, where the first protein is an immunoglobulin
CC molecule or its fragment and the second protein is non-immunoglobulin
CC target polypeptide each linked to the other directly or by a linker
CC molecule. The immunogenically modified fusion protein is useful in
CC combining known favourable properties of a composition or in creating new
CC properties of a composition which elicits biological or pharmacological
CC efficacy without having undesirable physiological effects such as nausea
CC or gastric upset. The present sequence is mouse 14.18 antibody modified
CC epitope. This sequence is used in the exemplification of the invention
XX
SQ Sequence 113 AA;

Query Match 94.6%; Score 561; DB 5; Length 113;
Best Local Similarity 94.7%; Pred. No. 1.5e-42;
Matches 107; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNNMWRQNIKSLWIGAIDPYYGTSY 60
Db 1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNNMWRQNIKSLWIGAIDPYYGTSY 60
QY 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDATVYVCVSGMEYWGQTSVTSS 113


```

XX AC ADG67527;
XX AC
XX DT 11-MAR-2004 (first entry)
XX DE
XX DE 14.18 antibody VH mouse modified epitope.
XX KW human; mouse; T-cell epitope; major histocompatibility complex; MHC;
XX KW immunogenicity; MHC class II; antibody.
XX OS Mus sp.
XX PN WO200269232-A2.
XX PD 06-SEP-2002.
XX PF 18-FEB-2002; 2002WO-EP001688.
XX PR 19-FEB-2001; 2001EP-00103954.
XX PR 08-MAR-2001; 2001EP-00105777.
XX PR 15-MAR-2001; 2001EP-00106536.
XX PR 15-MAR-2001; 2001EP-00106538.
XX PR 20-MAR-2001; 2001EP-00106899.
XX PR 20-MAR-2001; 2001EP-00107012.
XX PR 27-MAR-2001; 2001EP-00107568.
XX PR 25-APR-2001; 2001EP-00110220.
XX PR 30-MAY-2001; 2001EP-00113228.
XX PR 19-OCT-2001; 2001EP-00124965.
XX PR 12-NOV-2001; 2001EP-00126859.
XX PA (MERE ) MERCK PATENT GMBH.
XX PA Carr FJ, Carter G, Jones T, Williams S, Hamilton A;
XX PI WPI; 2002-750424/81.
XX DR
XX DR Identifying potential T-cell epitope peptides within the amino acid
XX PT sequence of a biological molecule, useful for preparing a biological
XX PT molecule with reduced immunogenicity, comprises determining peptide
XX PT binding to MHC molecules.
XX PS Example 21; Page 67; 85pp; English.
XX PS
XX CC The invention relates to a novel method for identifying one or more
XX CC potential T-cell epitope peptides within the amino acid sequence of a
XX CC biological molecule by determining the binding of the peptides to major
XX CC histocompatibility complex (MHC) molecules using in vitro or in silico
XX CC techniques or biological assays. The method of the invention is useful
XX CC for preparing a polypeptide, a protein, a fusion protein, an antibody or
XX CC their fragments with reduced immunogenicity. The potential T-cell epitope
XX CC peptide within the amino acid sequence of a parent immunogenically non-
XX CC modified biological molecule identified is useful for preparing a
XX CC biological molecule with reduced immunogenicity and having a retained
XX CC desired biological activity, where the T-cell epitope is a linear peptide.
XX CC The present sequence is used in the exemplification of the invention.
XX CC
XX SQ Sequence 113 AA;
XX SQ
Query Match 93.8%; Score 556; DB 5; Length 113;
Best Local Similarity 92.9%; Pred. No. 4,1e-42;
Matches 105; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
OY 1 EVQLVQSGAEVFKPGASVKISCKASGSSFTGYNNWVRQNIQKSLIEWIGALDIPYVGTSY 60
DB 1 EVQLQSGPELEKPSASVMISCKASGSSFTGYNNWVRQNIQKSLIEWIGALDIPYVGTSY 60
OY 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDVAVYCVSGMEYWGQGTSTVTVSS 113
DB 61 NQKFKGRATLTVDKSSSTAYMHLKSLTSEDSAVYCVSGMEYWGQGTSTVTVSS 113
RESULT 7
AAR11597

```

```

ID AAR11597 standard; protein; 153 AA.
XX AC AAR11597;
XX DT 14-JUN-1991 (first entry)
XX DE Murine monoclonal 14.18 H chain V region.
XX KW chimaeric binding protein; immunoglobulin; variable region; mouse.
XX OS Mus musculus.
XX PH Key Location/Qualifiers
XX FT Peptide 1..19
XX FT Protein /label= leader peptide
XX FT Region 20..153
XX FT Region 20..118
XX FT Region /label= variable region
XX FT Region 119..132
XX FT Region /label= J (H4)
XX FT Region 133..153
XX FT Region /label= constant region
XX PN WO9104329-A.
XX PD 04-APR-1991.
XX PF 20-SEP-1989; 89US-00409889.
XX PR 20-SEP-1989; 89US-00409889.
XX PA (ABBO ) ABBOTT LAB.
XX PI Gillies SD;
XX DR WPI; 1991-11/7518/16.
XX DR N-PSDB; AAQ11291.
XX PT Fusion protein prodn. - e.g. having dual biological activity, esp.
XX PT antibodies, by transfecting host cell with constructed cassette and
XX PT second DNA sequence.
XX PS Example; Fig 2; 52pp; English.
XX CC Two separate H and L chain cDNA libraries were prepared from mRNA
XX CC isolated from the murine hybridoma cell line 14.18. The lambda gt10
XX CC library was enriched for full-length L- and H-chains. It was screened by
XX CC filter hybridisation using various C region probes. Ten phage clones from
XX CC each screening were analysed further by restriction analysis. The longest
XX CC H cDNA sequence was sequenced. It appears to encode a normal length Ig
XX CC leader peptide. To ensure translation starts from the second ATG codon
XX CC once additional 5' sequences have been added to the insert, the cDNA is
XX CC truncated by limited Bal31 exonuclease treatment. An XhoI linker was then
XX CC added to give a sequence which, when expressed, will result in an mRNA
XX CC encoding a normal Ig leader sequence and a functional variable region.
XX CC The deduced amino acid sequence is given here. See also AAQ11292
XX SQ Sequence 153 AA;
XX SQ
Query Match 93.8%; Score 556; DB 2; Length 153;
Best Local Similarity 92.9%; Pred. No. 5,7e-42;
Matches 105; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
OY 1 EVQLVQSGAEVFKPGASVKISCKASGSSFTGYNNWVRQNIQKSLIEWIGALDIPYVGTSY 60
DB 20 EVQLQSGPELEKPSASVMISCKASGSSFTGYNNWVRQNIQKSLIEWIGALDIPYVGTSY 79
OY 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDVAVYCVSGMEYWGQGTSTVTVSS 113
DB 80 NQKFKGRATLTVDKSSSTAYMHLKSLTSEDSAVYCVSGMEYWGQGTSTVTVSS 132
RESULT 8

```

AAE27851
 ID AAE27851 standard; protein; 113 AA.
 AC AAE27851;
 XX
 DT 13-DEC-2002 (first entry)
 XX
 DE Mouse 14.18 antibody de-immunised VH5 modified epitope.
 XX
 KW Mouse; fusion protein; immunological; major histocompatibility complex;
 KW MHC; gastric upset; nausea; 14.18 antibody.
 XX
 OS Mus sp.
 XX
 PN WO200266514-A2.
 XX
 PD 29-AUG-2002.
 XX
 PF 18-FEB-2002; 2002WO-EP001690.
 XX
 PR 19-FEB-2001; 2001EP-00103955.
 PR 05-APR-2001; 2001EP-00108291.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Gillies S, Carr FJ, Jones T, Carter G, Hamilton A, Williams S;
 PI Hanlon M, Watkins J, Baker M, Way JC;
 XX
 DR WPI; 2002-667054/71.
 XX
 PT New modified fusion protein with reduced immunogenicity, useful for
 PT combining favorable properties of a composition, comprises an
 PT immunoglobulin molecule linked to a non-immunoglobulin target
 PT polypeptide.
 XX
 PS Example 19; Page 78; 92pp; English.
 XX
 CC The invention relates to an immunogenically modified fusion protein
 CC derived from a parent fusion protein, comprising first and second
 CC protein/polypeptides, where the first protein is an immunoglobulin
 CC molecule or its fragment and the second protein is a non-immunoglobulin
 CC target polypeptide each linked to the other directly or by a linker
 CC molecule. The immunogenically modified fusion protein is useful in
 CC combining known favourable properties of a composition or in creating new
 CC properties of a composition which elicits biological or pharmacological
 CC efficacy without having undesirable physiological effects such as nausea
 CC or gastric upset. The present sequence is mouse 14.18 antibody modified
 CC epitope. This sequence is used in the exemplification of the invention.
 XX
 SQ Sequence 113 AA;
 Query Match 90.4%; Score 536; DB 5; Length 113;
 Best Local Similarity 88.5%; Pred. No. 2.5e-40;
 Matches 100; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
 QY 1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNVQRNIQKSLWIGAIQDPYGGTSY 60
 DB 1 EVQLQSGPELKPKGASVKISCKASGSSFTGYNMNVQRNIQKSLWIGAIQDPYGGTSY 60
 QY 61 NQKPKGRATLTVDKSTSTAYMHLKSLRSEDATVYYCVSGMEYWGQTSVTSS 113
 DB 61 NQKPKGRVTITVDKSSQAYMHLKSLTSDTAVYYCVSGMEYWGQTSVTSS 113
 RESULT 9
 ADG67523
 ID ADG67523 standard; protein; 113 AA.
 XX
 AC ADG67523;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE 14.18 antibody de-immunised VH5 modified epitope.

XX
 KW human; mouse; T-cell epitope; major histocompatibility complex; MHC;
 KW immunogenicity; MHC class II; antibody.
 XX
 OS Unidentified.
 XX
 PN WO200269232-A2.
 XX
 PD 06-SEP-2002.
 XX
 PF 18-FEB-2002; 2002WO-EP001688.
 XX
 PR 19-FEB-2001; 2001EP-00103954.
 PR 08-MAR-2001; 2001EP-00105777.
 PR 15-MAR-2001; 2001EP-00106536.
 PR 15-MAR-2001; 2001EP-00106538.
 PR 20-MAR-2001; 2001EP-00106899.
 PR 20-MAR-2001; 2001EP-00107012.
 PR 27-MAR-2001; 2001EP-00107568.
 PR 25-APR-2001; 2001EP-00110220.
 PR 30-MAY-2001; 2001EP-00113228.
 PR 19-OCT-2001; 2001EP-00124965.
 PR 12-NOV-2001; 2001EP-00126859.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Carr FU, Carter G, Jones T, Williams S, Hamilton A;
 PI WPI; 2002-750424/81.
 XX
 PT Identifying potential T-cell epitope peptides within the amino acid
 PT sequence of a biological molecule, useful for preparing a biological
 PT molecule with reduced immunogenicity, comprises determining peptide
 PT binding to MHC molecules.
 XX
 PS Example 21; Page 66; 85pp; English.
 XX
 CC The invention relates to a novel method for identifying one or more
 CC potential T-cell epitope peptides within the amino acid sequence of a
 CC biological molecule by determining the binding of the peptides to major
 CC histocompatibility complex (MHC) molecules using in vitro or in silico
 CC techniques or biological assays. The method of the invention is useful
 CC for preparing a polypeptide, a protein, a fusion protein, an antibody or
 CC their fragments with reduced immunogenicity. The potential T-cell epitope
 CC peptide within the amino acid sequence of a parent immunogenically non-
 CC modified biological molecule identified is useful for preparing a
 CC biological molecule with reduced immunogenicity and having a retained
 CC desired biological activity, where the T-cell epitope is a linear peptide.
 CC The present sequence is used in the exemplification of the invention.
 XX
 SQ Sequence 113 AA;
 Query Match 90.4%; Score 536; DB 5; Length 113;
 Best Local Similarity 88.5%; Pred. No. 2.5e-40;
 Matches 100; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
 QY 1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNVQRNIQKSLWIGAIQDPYGGTSY 60
 DB 1 EVQLQSGPELKPKGASVKISCKASGSSFTGYNMNVQRNIQKSLWIGAIQDPYGGTSY 60
 QY 61 NQKPKGRATLTVDKSTSTAYMHLKSLRSEDATVYYCVSGMEYWGQTSVTSS 113
 DB 61 NQKPKGRVTITVDKSSQAYMHLKSLTSDTAVYYCVSGMEYWGQTSVTSS 113
 RESULT 10
 AAE27841
 ID AAE27841 standard; protein; 113 AA.
 XX
 AC AAE27841;
 XX
 DT 13-DEC-2002 (first entry)
 XX

DE Mouse 14.18 antibody VH modified epitope.
 XX
 XX Mouse; fusion protein; immunological; major histocompatibility complex;
 KW MHC; gastric upset; nausea; 14.18 antibody.
 XX
 OS Mus sp.
 XX
 XX WO200266514-A2.
 XX
 XX 29-AUG-2002.
 XX
 XX 18-FEB-2002; 2002WO-EP001690.
 XX
 XX 19-FEB-2001; 2001EP-00103955.
 XX
 XX 05-APR-2001; 2001EP-00108291.
 XX
 XX (MERE) MERCK PATENT GMBH.
 XX
 XX Gillies S, Carr FU, Jones T, Carter G, Hamilton A, Williams S;
 FI Hanlon M, Watkins J, Baker M, Way JC;
 XX WPI; 2002-667054/71.
 XX
 XX New modified fusion protein with reduced immunogenicity, useful for
 PT combining favorable properties of a composition, comprises an
 PT immunoglobulin molecule linked to a non-immunoglobulin target
 PT polypeptide.
 XX
 XX Example 19; Page 77; 92pp; English.
 XX
 XX The invention relates to an immunogenically modified fusion protein
 CC derived from a parent fusion protein, comprising first and second
 CC proteins/polypeptides, where the first protein is an immunoglobulin
 CC molecule or its fragment and the second protein is an immunoglobulin
 CC target polypeptide each linked to the other directly or by a linker
 CC molecule. The immunogenically modified fusion protein is useful in
 CC combining known favourable properties of a composition or in creating new
 CC properties of a composition which elicits biological or pharmacological
 CC efficacy without having undesirable physiological effects such as nausea
 CC or gastric upset. The present sequence is mouse 14.18 antibody modified
 CC epitope. This sequence is used in the exemplification of the invention.
 XX
 XX Sequence 113 AA;
 SQ
 Query Match 88.9%; Score 527; DB 5; Length 113;
 Best Local Similarity 87.6%; Pred. No. 1.6e-39;
 Matches 99; Conservative 8; Mismatches 6; Indels 0; Gaps 0;
 QY 1 EVQLVSGAEVEKPGASVKISCKASGSSFTGYNNWVRQNTGKSLIEWIGALDPYGGTYSY 60
 XX
 XX 1 EVQLVSGAEVEKPGASVKISCKASGSSFTGYNNWVRQNTGKSLIEWIGALDPYGGTYSY 60
 Db
 QY 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDYAVYCVSGMEYWGQGTSTVTVSS 113
 XX
 XX 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDYAVYCVSGMEYWGQGTSTVTVSS 113
 Db
 RESULT 11
 ADG67513
 ID ADG67513 standard; protein; 113 AA.
 XX
 XX ADG67513;
 AC
 XX 11-MAR-2004 (first entry)
 DT
 XX 14.18 antibody VH veneered modified epitope.
 DE
 XX human; mouse; T-cell epitope; major histocompatibility complex; MHC;
 KW immunogenicity; MHC class II; antibody.
 XX
 XX Unidentified.
 OS
 XX WO200269232-A2.
 FN

XX
 PD
 XX
 XX 06-SEP-2002.
 PF
 XX 18-FEB-2002; 2002WO-EP001688.
 XX
 XX 19-FEB-2001; 2001EP-00103954.
 PR
 XX 08-MAR-2001; 2001EP-00105777.
 PR
 XX 15-MAR-2001; 2001EP-00106536.
 PR
 XX 15-MAR-2001; 2001EP-00106538.
 PR
 XX 20-MAR-2001; 2001EP-00106899.
 PR
 XX 20-MAR-2001; 2001EP-00107012.
 PR
 XX 27-MAR-2001; 2001EP-00107568.
 PR
 XX 25-APR-2001; 2001EP-00110220.
 PR
 XX 30-MAY-2001; 2001EP-00113228.
 PR
 XX 19-OCT-2001; 2001EP-00124965.
 PR
 XX 12-NOV-2001; 2001EP-00126859.
 XX
 XX (MERE) MERCK PATENT GMBH.
 PA
 XX Carr FU, Carter G, Jones T, Williams S, Hamilton A;
 FI WPI; 2002-750424/81.
 XX
 XX Identifying potential T-cell epitope peptides within the amino acid
 PT sequence of a biological molecule, useful for preparing a biological
 PT molecule with reduced immunogenicity, comprises determining peptide
 PT binding to MHC molecules.
 XX
 XX Example 21; Page 65; 85pp; English.
 PS
 XX The invention relates to a novel method for identifying one or more
 CC potential T-cell epitope peptides within the amino acid sequence of a
 CC biological molecule by determining the binding of the peptides to major
 CC histocompatibility complex (MHC) molecules using in vitro or in silico
 CC techniques or biological assays. The method of the invention is useful
 CC for preparing a polypeptide, a protein, a fusion protein, an antibody or
 CC their fragments with reduced immunogenicity. The potential T-cell epitope
 CC peptide within the amino acid sequence of a parent immunogenically non-
 CC modified biological molecule identified is useful for preparing a
 CC modified biological molecule with reduced immunogenicity and having a retained
 CC desired biological activity, where the T-cell epitope is a 13mer peptide.
 CC The present sequence is used in the exemplification of the invention.
 XX
 XX Sequence 113 AA;
 SQ
 Query Match 88.9%; Score 527; DB 5; Length 113;
 Best Local Similarity 87.6%; Pred. No. 1.6e-39;
 Matches 99; Conservative 8; Mismatches 6; Indels 0; Gaps 0;
 QY 1 EVQLVSGAEVEKPGASVKISCKASGSSFTGYNNWVRQNTGKSLIEWIGALDPYGGTYSY 60
 XX
 XX 1 EVQLVSGAEVEKPGASVKISCKASGSSFTGYNNWVRQNTGKSLIEWIGALDPYGGTYSY 60
 Db
 QY 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDYAVYCVSGMEYWGQGTSTVTVSS 113
 XX
 XX 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDYAVYCVSGMEYWGQGTSTVTVSS 113
 Db
 RESULT 12
 AAE27849
 ID AAE27849 standard; protein; 113 AA.
 XX
 XX AAE27849;
 AC
 XX 13-DEC-2002 (first entry)
 DT
 XX Mouse 14.18 antibody de-immunised VH4 modified epitope.
 DE
 XX Mouse; fusion protein; immunological; major histocompatibility complex;
 KW MHC; gastric upset; nausea; 14.18 antibody.
 XX
 XX Unidentified.
 OS
 XX Mus sp.
 FN

PN WO200266514-A2.
 XX 29-AUG-2002.
 XX 18-FEB-2002; 2002WO-EP001690.
 XX 19-FEB-2001; 2001EP-00103955.
 PR 05-APR-2001; 2001EP-00108291.
 XX (MERE) MERCK PATENT GMBH.
 XX Gillies S, Carr FJ, Jones T, Carter G, Hamilton A, Williams S;
 PI Hanlon M, Watkins J, Baker M, Way JC;
 XX WPI; 2002-667054/71.
 XX New modified fusion protein with reduced immunogenicity, useful for
 PT combining favorable properties of a composition, comprises an
 PT immunoglobulin molecule linked to a non-immunoglobulin target
 PT polypeptide.
 XX Example 19; Page 78; 92pp; English.
 XX The invention relates to an immunogenically modified fusion protein
 CC derived from a parent fusion protein, comprising first and second
 CC proteins/polypeptides, where the first protein is an immunoglobulin
 CC molecule or its fragment and the second protein is non-immunoglobulin
 CC target polypeptide each linked to the other directly or by a linker
 CC molecule. The immunogenically modified fusion protein is useful in
 CC combining known favourable properties of a composition or in creating new
 CC properties of a composition which elicits biological or pharmacological
 CC efficacy without having undesirable physiological effects such as nausea
 CC or gastric upset. The present sequence is mouse 14.18 antibody modified
 CC epitope. This sequence is used in the exemplification of the invention.
 XX Sequence 113 AA;
 SQ

Query Match 88.4%; Score 524; DB 5; Length 113;
 Best Local Similarity 86.7%; Pred. No. 3e-39;
 Matches 98; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
 QY 1 EVQLVSGAEVKEPKGASVKISCKASGSSFTGYNNMNRQINIGKSLWIGALDIPYGGTSY 60
 DB 1 EVQLVSGAEVKEPKGASVKISCKASGSSFTGYNNMNRQINIGKSLWIGALDIPYGGTSY 60
 QY 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDATVYVCVSGMEYWGQTSVTSS 113
 DB 61 NQKFKGRVTITVDKSSQAYMHLKSLTSDTAVYVCVSGMEYWGQTTVTSS 113

RESULT 13
 ADG67521
 ID ADG67521 standard; protein; 113 AA.
 AC ADG67521;
 XX 11-MAR-2004 (first entry)
 XX 14.18 antibody de-immunised VH4 modified epitope.
 XX human; mouse; T-cell epitope; major histocompatibility complex; MHC;
 KW immunogenicity; MHC class II; antibody.
 XX Unidentified.
 OS
 XX WO200269232-A2.
 XX 06-SEP-2002.
 XX 18-FEB-2002; 2002WO-EP001688.
 XX 19-FEB-2001; 2001EP-00103954.
 PR 08-MAR-2001; 2001EP-00105777.

PR 15-MAR-2001; 2001EP-00106536.
 PR 15-MAR-2001; 2001EP-00106538.
 PR 20-MAR-2001; 2001EP-00106899.
 PR 20-MAR-2001; 2001EP-00107012.
 PR 27-MAR-2001; 2001EP-00107568.
 PR 25-APR-2001; 2001EP-00110220.
 PR 30-MAY-2001; 2001EP-00113228.
 PR 19-OCT-2001; 2001EP-00114965.
 PR 12-NOV-2001; 2001EP-00126859.
 XX (MERE) MERCK PATENT GMBH.
 XX Carr FJ, Carter G, Jones T, Williams S, Hamilton A;
 PI WPI; 2002-750424/81.
 XX Identifying potential T-cell epitope peptides within the amino acid
 PT sequence of a biological molecule, useful for preparing a biological
 PT molecule with reduced immunogenicity, comprises determining peptide
 PT binding to MHC molecules.
 XX Example 21; Page 66; 85pp; English.
 XX The invention relates to a novel method for identifying one or more
 CC potential T-cell epitope peptides within the amino acid sequence of a
 CC biological molecule by determining the binding of the peptides to major
 CC histocompatibility complex (MHC) molecules using in vitro or in silico
 CC techniques or biological assays. The method of the invention is useful
 CC for preparing a polypeptide, a protein, a fusion protein, an antibody or
 CC their fragments with reduced immunogenicity. The potential T-cell epitope
 CC peptide within the amino acid sequence of a parent immunogenically non-
 CC modified biological molecule identified is useful for preparing a
 CC biological molecule with reduced immunogenicity and having a retained
 CC desired biological activity, where the T-cell epitope is a 13mer peptide.
 CC The present sequence is used in the exemplification of the invention.
 XX Sequence 113 AA;
 SQ

Query Match 88.4%; Score 524; DB 5; Length 113;
 Best Local Similarity 86.7%; Pred. No. 3e-39;
 Matches 98; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
 QY 1 EVQLVSGAEVKEPKGASVKISCKASGSSFTGYNNMNRQINIGKSLWIGALDIPYGGTSY 60
 DB 1 EVQLVSGAEVKEPKGASVKISCKASGSSFTGYNNMNRQINIGKSLWIGALDIPYGGTSY 60
 QY 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDATVYVCVSGMEYWGQTSVTSS 113
 DB 61 NQKFKGRVTITVDKSSQAYMHLKSLTSDTAVYVCVSGMEYWGQTTVTSS 113

RESULT 14
 AAE27843
 ID AAE27843 standard; protein; 113 AA.
 XX AAE27843;
 XX 13-DEC-2002 (first entry)
 XX Mouse 14.18 antibody de-immunised VH1 modified epitope.
 XX Mouse; fusion protein; immunological; major histocompatibility complex;
 KW MHC; gastric upset; nausea; 14.18 antibody.
 XX Mus sp.
 OS
 XX WO200266514-A2.
 XX 29-AUG-2002.
 XX 18-FEB-2002; 2002WO-EP001690.
 PR 19-FEB-2001; 2001EP-00103955.

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PR 05-APR-2001; 2001EP-00108291.
PA (MERE ) MERCK PATENT GMBH.
PI Gillies S, Carr FJ, Jones T, Carter G, Hamilton A, Williams S;
PI Hanlon M, Watkins J, Baker M, Way JC;
XX WPI; 2002-667054/71.
XX
XX New modified fusion protein with reduced immunogenicity, useful for
XX combining favorable properties of a composition, comprises an
XX immunoglobulin molecule linked to a non-immunoglobulin target
XX polypeptide.
XX
XX Example 19; Page 77; 92pp; English.
XX
XX The invention relates to an immunogenically modified fusion protein
XX derived from a parent fusion protein, comprising first and second
XX proteins/polypeptides, where the first protein is an immunoglobulin
XX molecule or its fragment and the second protein is non-immunoglobulin
XX target polypeptide each linked to the other directly or by a linker
XX molecule. The immunogenically modified fusion protein is useful in
XX combining known favourable properties of a composition or in creating new
XX properties of a composition which elicits biological or pharmacological
XX efficacy without having undesirable physiological effects such as nausea
XX or gastric upset. The present sequence is mouse 14.18 antibody modified
XX epitope. This sequence is used in the exemplification of the invention.
XX
XX Sequence 113 AA;
SQ
Query Match 87.9%; Score 521; DB 5; Length 113;
Best Local Similarity 85.8%; Pred. No. 5.5e-39;
Matches 97; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
QY 1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNNWVRQNIKSLWIGALIDPYVGGTSY 60
DB 1 EVQLVQSGPELKPGASVKISCKASGSSFTGYNNWVRQNIKSLWIGALIDPYVGGTSY 60
QY 61 NQKFKGRATLTVDKSTSTAYNHLKSLRSEDVAVYVCVSGMEYWGQGTSTVTVSS 113
DB 61 NQKFKSRVTITADKSSQAYNHLKSLTSEDVAVYVCVSGMEYWGQGTSTVTVSS 113
RESULT 15
ADG67515
ID ADG67515 standard; protein; 113 AA.
AC
XX ADG67515;
XX
XX 11-MAR-2004 (first entry)
XX
XX 14.18 antibody de-immunised VH1 modified epitope.
XX
XX human; mouse; T-cell epitope; major histocompatibility complex; MHC;
XX immunogenicity; MHC class II; antibody.
XX
XX Unidentified.
XX
XX WO200269232-A2.
XX
XX 06-SEP-2002.
XX
XX 18-FEB-2002; 2002WO-EP001688.
XX
XX 19-FEB-2001; 2001EP-00103954.
XX
XX 08-MAR-2001; 2001EP-00105777.
XX
XX 15-MAR-2001; 2001EP-00106536.
XX
XX 15-MAR-2001; 2001EP-00106538.
XX
XX 20-MAR-2001; 2001EP-00106899.
XX
XX 20-MAR-2001; 2001EP-00107012.
XX
XX 27-MAR-2001; 2001EP-00107568.
XX
XX 25-APR-2001; 2001EP-00110220.
XX
XX 30-MAY-2001; 2001EP-00113228.

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PR 19-OCT-2001; 2001EP-00124965.
PR 12-NOV-2001; 2001EP-00126859.
XX
XX (MERE ) MERCK PATENT GMBH.
XX
XX Carr FJ, Carter G, Jones T, Williams S, Hamilton A;
XX WPI; 2002-750424/81.
XX
XX Identifying potential T-cell epitope peptides within the amino acid
XX sequence of a biological molecule, useful for preparing a biological
XX molecule with reduced immunogenicity, comprises determining peptide
XX binding to MHC molecules.
XX
XX Example 21; Page 66; 85pp; English.
XX
XX The invention relates to a novel method for identifying one or more
XX potential T-cell epitope peptides within the amino acid sequence of a
XX biological molecule by determining the binding of the peptides to major
XX histocompatibility complex (MHC) molecules using in vitro or in silico
XX techniques or biological assays. The method of the invention is useful
XX for preparing a polypeptide, a protein, a fusion protein, an antibody or
XX their fragments with reduced immunogenicity. The potential T-cell epitope
XX peptide within the amino acid sequence of a parent immunogenically non-
XX modified biological molecule identified is useful for preparing a
XX biological molecule with reduced immunogenicity and having a retained
XX desired biological activity, where the T-cell epitope is a 13mer peptide.
XX The present sequence is used in the exemplification of the invention.
XX
XX Sequence 113 AA;
SQ
Query Match 87.9%; Score 521; DB 5; Length 113;
Best Local Similarity 85.8%; Pred. No. 5.5e-39;
Matches 97; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
QY 1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNNWVRQNIKSLWIGALIDPYVGGTSY 60
DB 1 EVQLVQSGPELKPGASVKISCKASGSSFTGYNNWVRQNIKSLWIGALIDPYVGGTSY 60
QY 61 NQKFKGRATLTVDKSTSTAYNHLKSLRSEDVAVYVCVSGMEYWGQGTSTVTVSS 113
DB 61 NQKFKSRVTITADKSSQAYNHLKSLTSEDVAVYVCVSGMEYWGQGTSTVTVSS 113
Search completed: April 18, 2005, 10:00:58
Job time : 64 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 09:57:11 ; Search time 11.5 Seconds
(without alignments)
945.434 Million cell updates/sec

Title: US-10-737-208A-2

Perfect score: 593
Sequence: 1 EVQLVQSGAEVEKPGASVKI.....YYCVSGMEYWGQTSVTVSS 113

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	471.5	79.5	137	2 H32513	Ig heavy chain pre
2	467.5	78.8	119	2 F30502	Ig heavy chain v r
3	459	77.4	118	2 PL0200	anti-DNA autoantib
4	441.5	74.5	118	2 PL0084	Ig heavy chain v r
5	440.5	74.3	150	2 PN0444	Ig heavy chain v r
6	427.5	72.1	112	2 S09957	Ig heavy chain v-D
7	426.5	71.9	114	2 S26319	Ig heavy chain v r
8	426.5	71.9	139	2 A27609	Ig heavy chain pre
9	425.5	71.8	135	2 PS0057	Ig heavy chain pre
10	424.5	71.6	120	2 E45722	anti-glycoprotein
11	424	71.5	151	2 PL0011	Ig heavy chain pre
12	423.5	71.4	118	1 MHMS38	Ig heavy chain v r
13	418.5	70.6	128	2 I37267	Ig heavy chain v r
14	417.5	70.4	128	2 S36265	Ig heavy chain v r
15	416	70.2	119	2 PH0099	Ig heavy chain v r
16	414	69.8	117	1 MHMS4E	Ig heavy chain v r
17	414	69.8	140	2 T01407	Ig heavy chain (my
18	412	69.5	117	1 MHMSJ5	Ig heavy chain v r
19	410.5	69.2	120	2 S41394	Ig heavy chain v r
20	410.5	69.2	135	2 S49530	anti-Sm antibody V
21	409	69.0	116	2 S55542	Ig heavy chain v r
22	409	69.0	119	2 B53285	Ig heavy chain v a
23	409	69.0	125	2 PH0100	Ig heavy chain v r
24	409	69.0	142	2 A32483	Ig heavy chain v r
25	408.5	68.9	120	2 F45722	anti-glycoprotein
26	408	68.8	107	2 PH0971	Ig heavy chain v r
27	406.5	68.5	136	2 JL0077	Ig heavy chain pre
28	406	68.5	119	2 PH0961	Ig heavy chain v r
29	406	68.5	138	2 PH0105	anti-digoxin trans

30	405.5	68.4	120	2 PH0962	Ig heavy chain v r
31	404.5	68.2	120	2 A49982	Ig heavy chain v r
32	404.5	68.2	122	2 PH0958	Ig heavy chain v r
33	404.5	68.2	122	2 PH0887	Ig heavy chain v r
34	403.5	68.0	128	2 C37267	Ig heavy chain v r
35	402.5	67.9	139	1 MHMS18	Ig heavy chain pre
36	402.5	67.9	287	4 PC4402	pelB leader/Ig hea
37	401.5	67.7	128	2 PH0952	Ig heavy chain v r
38	401.5	67.7	131	2 S65537	Ig heavy chain v r
39	401.5	67.7	136	2 PH0960	Ig heavy chain v r
40	401	67.6	129	2 A33548	Ig heavy chain v-1
41	401	67.6	140	2 S04575	Ig heavy chain pre
42	400	67.5	133	2 C33548	Ig heavy chain v-1
43	400	67.5	627	2 S14683	Ig mu chain precu
44	399.5	67.4	132	2 PH0954	Ig heavy chain v r
45	399.5	67.4	139	2 PS0024	Ig heavy chain pre

ALIGNMENTS

RESULT 1

H32513

Ig heavy chain precursor V region (BXW16) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000

C:Accession: H32513

R:Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;

J. Clin. Invest. 82, 852-860, 1988

A:Title: Immunoglobulin kappa light chain variable region gene complex organization and

A:Reference number: A94689; MUID:88331394; PMID:3138286

A:Accession: H32513

A:Molecule type: DNA

A:Residues: 1-137 <KOF>

A:Cross-references: GB:M20831; NID:gl96949; PIDN:AAA38848.1; PID:gl96950

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 79.5%; Score 471.5; DB 2; Length 137;

Best Local Similarity 76.3%; Pred. No. 6.3e-36;

Matches 90; Conservative 11; Mismatches 12; Indels 5; Gaps 1;

QY 1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMVRQNIKSLKLEWIGAIPIYGGTSY 60

Db 20 ETQLQSGAELVKPGASVKISCKASGYSFTGYNMVRQSHKSLKLEWIGAIPIYGGTSY 79

QY 61 NQKPKGRATLTVDKSTSTAYMHLKSLRSEDATVYVCV-----SGMEYWGQTSVTVSS 113

Db 80 NQKPKGRATLTVDKSSSTAYMQLNLSLTSDSAIVYCARKNYGSFDFWQGQTTLTVSS 137

RESULT 2

F30502

Ig heavy chain V region (A52) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000

C:Accession: F30502

R:Filat, D.; Webster, D.M.; Rees, A.R.

J. Immunol. 141, 1745-1753, 1988

A:Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 m

A:Reference number: A30502; MUID:88315787; PMID:2457627

A:Accession: F30502

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-119 <EIL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 78.8%; Score 467.5; DB 2; Length 119;

Matches 89; Conservative 11; Mismatches 12; Indels 7; Gaps 1;

QY 1 EVOLVQSGAEVEKPGASVKISCKASGSSFTGYNNWVRQNIKGSLEWIGAIIDPYVGGTSY 60
Db 1 EIQLQQSGAELVKGASVKISCKASGYSTGYNNWVKQSHGKSLWIGKINPYVGGTSY 60
QY 61 NQKFKGRATLTVDKSTAYMHLKSLRSEDATVYCVSG-----MEYWGQGTSTVTS 112
Db 61 NQKFKGRATLTVDKSSSTAYMQLNSLTSDSAVYVCARGLRGGYFDYWGQGTTLTVS 119

RESULT 3
PNO200
Ig heavy chain V region precursor - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: PLO200
R:Smith, R.G.; Voss Jr., E.W.
Mol. Immunol. 27, 463-470, 1990
A:Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from N
A:Reference number: PLO198; MUID:90309768; PMID:2114528
A:Accession: PLO200
A:Molecule type: mRNA
A:Residues: 1-118 <SMI>
A:Cross-references: GB:X53641; NID:G50193; PIDN:CAA37692.1; PID:G930139
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:50-66/Region: complementarity-determining 2
F:99-110/Region: complementarity-determining 3
F:99-106/Region: D region
F:107-118/Region: JH region

Query Match 77.4%; Score 459; DB 2; Length 118;
Best Local Similarity 74.6%; Pred. No. 7.3e-35;
Matches 88; Conservative 10; Mismatches 12; Indels 8; Gaps 1;

QY 1 EVOLVQSGAEVEKPGASVKISCKASGSSFTGYNNWVRQNIKGSLEWIGAIIDPYVGGTSY 60
Db 1 EIQLQQSGAELVKGASVKISCKASGYSTGYNNWVKQSHGKSLWIGKINPYVGGTSY 60
QY 61 NQKFKGRATLTVDKSTAYMHLKSLRSEDATVYCVSG-----EYWGQGTSTV 110
Db 61 NQKFKGRATLTVDKSSSTAYMQLNSLTSDSAVYVCARGITTRTFAYWGQGTTLTV 118

RESULT 4
PLO084
Ig heavy chain V region (E4) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 21-Jan-2000
C:Accession: PLO084
R:Meek, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.; Ca
J. Exp. Med. 169, 519-533, 1989
A:Title: Structural characterization of antiidiotypic antibodies; evidence that Ab2s are
A:Reference number: PLO080; MUID:89094248; PMID:2492056
A:Accession: PLO084
A:Molecule type: mRNA
A:Residues: 1-118 <MEE>
A:Cross-references: GB:X58595; GB:Y00794; NID:G51573; PIDN:CAA41470.1; PID:G938254
A:Experimental source: strain BALB/c
A:Note: 66-Gly is translated as "X" from the codon GGN
A:Note: the sequence shown here is from the VH region of an antiidiotypic monoclonal ant
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.5%; Score 441.5; DB 2; Length 118;
Best Local Similarity 72.0%; Pred. No. 2.8e-33;
Matches 85; Conservative 12; Mismatches 16; Indels 5; Gaps 1;

QY 1 EVOLVQSGAEVEKPGASVKISCKASGSSFTGYNNWVRQNIKGSLEWIGAIIDPYVGGTSY 60
Db 1 EVOLQQSXXELEKPGASVKISCKASGYSTGYNNWVKQSHGKSLWIGKINPYVGGT 60

QY 61 NQKFKGRATLTVDKSTAYMHLKSLRSEDATVYCVSGM-----EYWGQGTSTVTS 113
Db 61 NQKFKGRATLTVDKSSSTAYMQLKSLTSDSAVYVCARGSSGYDYWGQGTTLTVS 118

RESULT 5
PNO444
Ig heavy chain V region precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PNO444
R:Kaluzs, B.; Betz, G.; Shao, H.; Diamantstein, T.; Weidle, U.H.
Gene 122, 321-328, 1992
A:Title: A general method for chimerization of monoclonal antibodies by inverse polymera
A:Reference number: PNO444; MUID:93138402; PMID:1339379
A:Accession: PNO444
A:Molecule type: mRNA
A:Residues: 1-150 <KAL>
A:Cross-references: GB:L02346
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-150/Product: Ig heavy chain V region #status predicted <MAT>
F:20-117/Domain: variable region <VRG>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 74.3%; Score 440.5; DB 2; Length 150;
Best Local Similarity 72.9%; Pred. No. 4.5e-33;
Matches 86; Conservative 11; Mismatches 16; Indels 5; Gaps 1;

QY 1 EVOLVQSGAEVEKPGASVKISCKASGSSFTGYNNWVRQNIKGSLEWIGAIIDPYVGGTSY 60
Db 20 EVLQQFGAELVKGFTSVKISCKASGYFTDYNNDWVKQSHGKSLWIGIDIDPNDSSSY 79
QY 61 NQKFKGRATLTVDKSTAYMHLKSLRSEDATVYCVS-----GMEYWGQGTSTVTS 113
Db 80 NQKFKGRATLTVDKSSSTAYMELSLTSDATVYVCARGFPYWGQGTSTVTS 137

RESULT 6
S09957
Ig heavy chain V-D-J region (106-10E) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 23-Jul-1999
C:Accession: S09957
R:Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
Eur. J. Immunol. 20, 771-777, 1990
A:Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie
A:Reference number: S09955; MUID:90269328; PMID:2347362
A:Accession: S09957
A:Molecule type: mRNA
A:Residues: 1-112 <REI>
A:Cross-references: EMBL:X51845; NID:G55244; PIDN:CAA36138.1; PID:G930213
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 72.1%; Score 427.5; DB 2; Length 112;
Best Local Similarity 73.5%; Pred. No. 5e-32;
Matches 83; Conservative 12; Mismatches 17; Indels 1; Gaps 1;

QY 1 EVOLVQSGAEVEKPGASVKISCKASGSSFTGYNNWVRQNIKGSLEWIGAIIDPYVGGTSY 60
Db 1 EVLQQSGPELVKSGASVKMSCKASGYFTDYNWVKQSHGKSLWIGVNSNGTSTY 60
QY 61 NQKFKGRATLTVDKSTAYMHLKSLRSEDATVYCVSGMEYWGQGTSTVTS 113
Db 61 NQKFKGRATLTVDKSLSTAYMQLNSLTSDSAVYVCARG-DYWGQGTTLTVS 112

RESULT 7
S26319
Ig heavy chain V region precursor - mouse (fragment)


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A:Reference number: PS0057; MUID:89197817; PMID:2467902
A:Accession: PS0057
A:Molecule type: DNA
A:Residues: 1-135 <BAO>
A:Cross-references: GB:D00307; NID:g220448; PIDN:BARA00213.1; PID:g220449
A:Note: the authors translated the codon AAG for residue 32 as Asn and GAC for 92 as Gl;
C:Comment: the gene encoding this protein was isolated from a hybridoma that produces a
C:Superfamily: immunoglobulin v region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-135/Product: Ig heavy chain v region PAR #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match          71.8%; Score 425.5; DB 2; Length 135;
Best Local Similarity 73.3%; Pred. No. 9.3e-32;
Matches 85; Conservative 10; Mismatches 18; Indels 3; Gaps 1;

Qy      1  EVQLVQSGAEVEKPGASVKISCKASGSSFTGTNNWVRQNIKSLIEWIGALDPYGGTSY 60
      Db      20  EVQLQQSGPELVKPGASVKISCKASGYSFTGTFMNWKQSHGKSLIEWIGRINPYNGDTTF 79

Qy      61  NQKFKGRATLTVDKSTSTAYMHLKSLRSDDTAVYCVS--GMKEYGQGTSTVTSS 113
      Db      80  NQKFKGKATLTVDKSSSTAHMERLSLTSDSAVYICARLNRYGAYWQGTLTVTSA 135

RESULT 10

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anti-glycoprotein in monoclonal antibody heavy-chain variable domain (Wad 3) - mouse (1)
 C:Species: Mus musculus (house mouse)
 C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: E45722
 R:R.Simpson, J.A.; Chow, J.C.; Baker, J.; Avdaloovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vaseq
 J. Virol. 67, 489-496, 1993
 A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on h
 A:Reference number: A45722; MUID:93100833; PMID:7677958
 A:Accession: E45722
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-120 <SIM>
 A:Note: sequence extracted from NCBI backbone (NCBIP:120593)
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: glycoprotein
 F:15-99/Domain: immunoglobulin homology <IMW>
 Query Match 71.6%; Score 424.5; DB 2; Length 120;
 Best Local Similarity 70.8%; Pred. No.1e-31;
 Matches 85; Conservative 12; Mismatches 16; Indels 7; Gaps 2;
 OV 1 EVOLVSGAEVKPGASVKISKSGSFTGMNVMVNRONIKSLSEWIG-AIDPYVGGTS 59

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Db      1  EVLQQSGPELVKPGASMKISCKASVYFTGYTMWVVKQSHQCNLEWLGIIINPYNGGTS  60
      QY    60  YNQKFKGRATLTVDKSTSTAYNHLKSLRASEDTAVYYCVS-----GMEYWGQGTSTVTVSS  113
      Db    61  YNQKFKGRATLTVDKSSNTAYNELLSLTSADSAVIYCTRRGFRDYMDYWGQGTSTVTVSS  120

RESULT 11
P00011
IG heavy chain precursor V region (4C11) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C:Accession: P00011
R:Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.
Mol. Immunol. 25, 33-40, 1988
A:Title: Structural basis of stimulatory anti-idiotypic antibodies.
A:Reference number: P00011; MUID:88142863; PMID:3125424
A:Accession: P00011
A:Molecule type: mRNA
A:Residues: 1-151 -CHE>
A:Experimental source: cell line 4C11
C:Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylch

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C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-136/Product: Ig heavy chain V region 4C11 #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>
F:50-54/Region: complementarity-determining 1
F:69-85/Region: complementarity-determining 2
F:118-125/Region: complementarity-determining 3
F:137-151/Domain: C region (fragment) #status predicted <COR>

Query Match 71.5%; Score 424; DB 2; Length 151;
Best Local Similarity 70.1%; Pred. No. 1,4e-31;
Matches 82; Conservative 13; Mismatches 18; Indels 4; Gaps 1;

QY 1 EVQLVQSGAEVEKPGASVKISCKASGSGFTGYNNWVRQNIKSLIEWIGAIIDPYVGGTSY 60
Db 20 EVQLQSGPELVKPGASVKISCKASGVTFTDYTHWVKQSHGKSLIEWIGGFDPNYDNTFY 79
QY 61 NQKFQKRALITVDKSTSTAYMHLKSLRSEDPAVYCVS----GMEYWGQGTSTVTVSS 113
Db 80 NEKFQKRALITVDKSSITAYMELRSLTSEDSAVYCYSDYDYGALDYGQGTSTVTVSS 136

RESULT 12
MHMS38
IG heavy chain V region (AC38 205.12) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C:Accession: A02040
R:Dildrop, R.; Bovens, J.; Siekevitz, M.; Beyreuther, K.; Rajewsky, K.
EMBO J. 3, 517-523, 1984
A:Title: A V region determinant (idiotope) expressed at high frequency in B lymphocytes
A:Reference number: A91000; MUID:84182519; PMID:6201362
A:Accession: A02040
A:Molecule type: protein
A:Residues: 1-118 <DIL>
A:Cross-references: UNIPROT:P06330
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-98/Region: V segment
F:15-98/Domain: immunoglobulin homology <IMM>
F:95-104/Region: D segment
F:105-118/Region: J segment
F:12-96/Disulfide bonds: #status predicted

Query Match 71.4%; Score 423.5; DB 1; Length 118;
Best Local Similarity 71.2%; Pred. No. 1.2e-31;
Matches 84; Conservative 10; Mismatches 19; Indels 5; Gaps 1;

QY 1 EVQLVQSGAEVEKPGASVKISCKASGSGFTGYNNWVRQNIKSLIEWIGAIIDPYVGGTSY 60
Db 1 EVQLQSGPELVKPGASVKISCKASGVTFTDYTHWVKQSHGKSLIEWIGDIPNNGGTSY 60
QY 61 NQKFQKRALITVDKSTSTAYMHLKSLRSEDPAVYCVSGMEY----WGQGTSTVTVSS 113
Db 61 NQKFQKRALITVDKSSITAYMELRSLTSEDSAVYCYARGYDPAVWGGTSTVTVSS 118

RESULT 13
I37267
IG heavy chain V region (129) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 16-Aug-1996
C:Accession: I37267
R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A:Title: Heavy and light chain variable region sequences and antibody properties of anti-
A:Reference number: A38740; MUID:91177923; PMID:1706720
A:Accession: I37267
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-128 <RUF>
C:Superfamily: immunoglobulin V region; immunoglobulin homology

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Best Local Similarity 70.1%; Pred. No. 5.9e-31;
Matches 82; Conservative 13; Mismatches 18; Indels 4; Gaps 1;
QY 1 EVOLVOSGAEEKPGASVKISKASGSSFTGYNMWVRQNIKSKLEWIGALIDPYIGTSY 60
Db 1 EVOLQOSGPPELVEFGASMKISKASGYSPAGYTMWVKQSHGKNLEWIGLINPYDGIAT 60
QY 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYCVSG---MEYWGQGTSTVTVSS 113
Db 61 NQKFKGKATLTVDKSSSTAYMDLLSLTSEDSAVYVCARGYVAVDYWGQGTSTVTVSS 117

Search completed: April 18, 2005, 10:06:47
Job time : 12.5 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 09:42:15 ; Search time 84.5 Seconds
(without alignments)
684,792 Million cell updates/sec

Title: US-10-737-208A-2
Perfect score: 593
Sequence: 1 EVQLVQSGAEVEKPGASVKI.....YYCVSGMEYWGQTSVTSS 113

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	477	80.4	120	Q920E8	Q920E8 mus musculus
2	436	73.5	123	Q8VIJ1	Q8VIJ1 mus musculus
3	435	73.4	117	Q9QXE9	Q9QXE9 mus musculus
4	423.5	71.4	118	HV51 MOUSE	P06330 mus musculus
5	423	71.3	117	Q9QXF0	Q9QXF0 mus musculus
6	423	71.3	134	Q65ZR6	Q65ZR6 mus musculus
7	416	70.2	470	Q7TWR1	Q7TWR1 mus musculus
8	415.5	70.1	488	Q91WR1	P01756 mus musculus
9	414	69.8	117	HV12 MOUSE	Q8K172 mus musculus
10	413.5	69.7	482	Q924R0	Q924R0 mus musculus
11	412.5	69.6	143	Q924R0	P01757 mus musculus
12	412	69.5	117	HV13 MOUSE	Q924G6 mus musculus
13	411.5	69.4	145	Q924Q6	Q924G9 mus musculus
14	411.5	69.4	145	Q924Q9	Q924R1 mus musculus
15	411.5	69.4	145	Q924R1	Q924R4 mus musculus
16	411.5	69.4	145	Q924R4	Q924G3 mus musculus
17	411	69.3	146	Q924Q3	Q924R0 mus musculus
18	409	69.0	119	Q9GYZ2	Q9GYZ2 schistosoma
19	409	69.0	142	Q924Q1	Q924G1 mus musculus
20	408	68.8	140	Q924R2	Q924R2 mus musculus
21	407.5	68.7	124	Q9UL92	Q9UL92 homo sapien
22	407	68.6	472	Q6PJA7	Q6PJA7 mus musculus
23	405.5	68.4	145	Q924P7	Q924P7 mus musculus
24	403.5	68.0	481	Q8BVCV5	Q8BVCV5 mus musculus
25	403	68.0	146	Q924Q8	Q924G8 mus musculus
26	402.5	67.9	137	Q924R6	Q924R6 mus musculus
27	402.5	67.9	139	HV07 MOUSE	P01751 mus musculus
28	402.5	67.9	145	Q924Q7	Q924G7 mus musculus
29	400.5	67.5	139	Q924R5	Q924R5 mus musculus
30	400.5	67.5	141	Q924Q4	Q924Q4 mus musculus
31	400	67.5	146	Q924R8	Q924R8 mus musculus

32	397.5	67.0	145	2	Q924R3	Q924R3 mus musculus
33	396	66.8	144	2	Q924P5	Q924P5 mus musculus
34	395.5	66.7	143	2	Q924P9	Q924P9 mus musculus
35	395.5	66.7	488	2	Q8K0F2	Q8K0F2 mus musculus
36	394.5	66.5	143	2	Q924Q5	Q924Q5 mus musculus
37	394.5	66.5	143	2	Q924R7	Q924R7 mus musculus
38	393	66.3	473	2	Q9D8L4	Q9D8L4 mus musculus
39	392.5	66.2	465	2	Q6FJB2	Q6FJB2 mus musculus
40	390	65.8	142	2	Q924Q2	Q924Q2 mus musculus
41	389.5	65.7	143	2	Q91VA2	Q91VA2 mus musculus
42	388.5	65.5	463	2	Q99LC4	Q99LC4 mus musculus
43	387.5	65.3	143	2	Q924P6	Q924P6 mus musculus
44	386.5	65.2	137	1	HV11 MOUSE	P01755 mus musculus
45	385.5	65.0	159	2	Q96QSO	Q96QSO homo sapien

ALIGNMENTS

RESULT 1

Q920E8	PRELIMINARY;	PRT;	120 AA.
AC	Q920E8;		
DT	01-DEC-2001 (Tremblrel. 19, Created)		
DT	01-DEC-2001 (Tremblrel. 19, Last sequence update)		
DT	01-OCT-2003 (Tremblrel. 25, Last annotation update)		
DE	Pterin-mimicking anti-idiotope heavy chain variable region (Fragment).		
DE	Mus musculus (Mouse).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Atkin J.D., Ispe A., Jennings I.G., Horaitis O., Cotton R.G.H.;		
RL	Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF307936; AAL09420.1; -.		
DR	HSSP; P01751; INQB.		
DR	SMART; SM00406; IGV; 1.		
DR	PROSITE; PS50835; IG_LIKE; 1.		
FT	NON_TER 1_1		
FT	NON_TER 120 120		
SQ	SEQUENCE 120 AA; 13204 MW; DC483AB1DE56F3C CRC64;		

Query Match 80.4%; Score 477; DB 2; Length 120;
Best Local Similarity 77.5%; Pred. No. 2.2e-41;
Matches 93; Conservative 7; Mismatches 12; Indels 8; Gaps 1;

QY	1	EVQLVQSGAEVEKPGASVKISCKASGSGFTGYNNMVRQNIKSLWIGAIIDPYGGTSY 60
Db	1	EVQLVQSGAEVEKPGASVKISCKASGSGFTGYNNMVRQNIKSLWIGAIIDPYGGTSY 60
QY	61	NOKFGKATLTVDKSTSTAYMHLKSLRSDTAVYCV-----SGMEYWGQTSVTYS 112
Db	61	NOKFGKATLTVDKSSSTAYMQLKSLTSDSAVYCAVYYGNSPAWFAYGQGLTVTS 120

RESULT 2

Q8VIJ1	PRELIMINARY;	PRT;	123 AA.
ID	Q8VIJ1		
AC	Q8VIJ1;		
DT	01-MAR-2002 (Tremblrel. 20, Created)		
DT	01-MAR-2002 (Tremblrel. 20, Last sequence update)		
DT	01-OCT-2003 (Tremblrel. 25, Last annotation update)		
DE	Anti-DNA heavy chain (Fragment).		
DE	Name=J558;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C3H/HeJ-lpr-lpr;		

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RX MEDLINE=96409289; PubMed=8814271;
RA Wloch M.K., Alexander A.L., Phippen A.M., Pisetsky D.S., Gilkeson G.S.;
RT "Differences in V kappa gene utilization and VH CDR3 sequence among
RL anti-DNA from C3H-Ipr mice and lupus mice with nephritis.";
DR Eur. J. Immunol. 26:2225-2233(1996).
DR EMBL; U59154; AAB02916.1; -.
DR HSP; P01751; INQB.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 123
FT NON_TER 123
SQ SEQUENCE 123 AA; 13806 MW; CC0037A806B59911E CRC64;

Query Match 73.5%; Score 436; DB 2; Length 123;
Best Local Similarity 68.3%; Pred. No. 3.8e-37;
Matches 86; Conservative 11; Mismatches 18; Indels 10; Gaps 1;

QY 1 EVQLVQSGAEVKEPKGASVKISCKASGSSFTGYNNWVRQNIKSLRWIGAIIDPYGTSY 60
DB 1 EIQLQSGTGLVKEPKGASVKISCKASGVSFTGYNNWVRQNIKSLRWIGAIIDPYGTSY 60
QY 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDATVYCVSG-----MEYWGQTSVT 110
DB 61 SQKFKGKATLTVDKSSRTATYMQNLSTSDSAVYVCARDYTYTYDEGCFAYWGQTLVT 120
QY 111 VSS 113
DB 121 VSA 123

RESULT 3
QYQX9E PRELIMINARY; PRT; 117 AA.
AC QYQX9E
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Immunoglobulin heavy chain V-D-J region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RA Clemens A., Rademaekers A., Specht C., Koelsch E.;
RA Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ225174; CAB65237.1; -.
DR PIR; F33932; F33932.
DR HSP; P01751; INQB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IGV.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13000 MW; CDDE2AF84D499734 CRC64;

Query Match 73.4%; Score 435; DB 2; Length 117;
Best Local Similarity 73.5%; Pred. No. 4.6e-37;
Matches 86; Conservative 10; Mismatches 17; Indels 4; Gaps 1;

QY 1 EVQLVQSGAEVKEPKGASVKISCKASGSSFTGYNNWVRQNIKSLRWIGAIIDPYGTSY 60
DB 1 EVQLQSGPELVKPGASVKMSCKASGYTFTDYNNWVRQNIKSLRWIGAIIDPYGTSY 60
QY 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDATVYCVS-----GMFYWGQTSVTSS 113
DB 61 NQKFKGKATLTVDKSSRTATYMQNLSTSDSAVYVCARDYTYTYDEGCFAYWGQTSVTSS 117

RESULT 4
HV51_MOUSE
ID HV51_MOUSE STANDARD; PRT; 118 AA.

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AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR; A02040; MEMS38.
DR HSP; P01751; INQB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IGV.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 98
FT DOMAIN 99 104 D segment.
FT DOMAIN 105 118 J segment.
FT DISULFID 22 96 By similarity.
FT NON_TER 118
SQ SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;

Query Match 71.4%; Score 423.5; DB 1; Length 118;
Best Local Similarity 71.2%; Pred. No. 7.1e-36;
Matches 84; Conservative 10; Mismatches 19; Indels 5; Gaps 1;

QY 1 EVQLVQSGAEVKEPKGASVKISCKASGSSFTGYNNWVRQNIKSLRWIGAIIDPYGTSY 60
DB 1 EVQLQSGPELVKPGASVKISCKASGYTFTDYNNWVRQNIKSLRWIGAIIDPYGTSY 60
QY 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDATVYCVSGMEY-----WGQTSVTSS 113
DB 61 NQKFKGKATLTVDKSSRTATYMQNLSTSDSAVYVCARGYDFFDVGWGTGTTVSS 118

RESULT 5
QYQXFO PRELIMINARY; PRT; 117 AA.
AC QYQXFO
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Immunoglobulin heavy chain V-D-J region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RA Clemens A., Rademaekers A., Specht C., Koelsch E.;
RA Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ225171; CAB65236.1; -.
DR PIR; PH0973; PH0973.
DR HSP; P01751; INQB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IGV.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13060 MW; D816AD0858A47E4C CRC64;

Query Match 71.3%; Score 423; DB 2; Length 117;
Best Local Similarity 70.9%; Pred. No. 8e-36;

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```
Matches 83; Conservative 12; Mismatches 18; Indels 4; Gaps 1;
QY 1 EVOLVOSGAEEVPGASVKISCKASGSSFTGYNNMVRQNIKSLWIGALIDPYVGGTSY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVOLQSGPELVKPGASVKMSCKASGYTFDYMKVWKQSHGKSLWIGIDINPNNGTSY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDVAVYCVSG---MEYWGQGTSTVTS 113
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVVYCARDKYDFYDWGQGTTLTVSS 117
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 6
Q65ZR6 PRELIMINARY; PRT; 134 AA.
AC Q65ZR6;
DT 25-OCT-2004 (TEMBLrel. 28, Created)
DT 25-OCT-2004 (TEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TEMBLrel. 28, Last annotation update)
DE Ab 126.33 heavy chain variable and joining regions (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91237115; PubMed=1709665;
RA Rueff-Juy D., Marche P.N., Drapier A.-M., Cazenave P.-A.;
RT "Junctional diversity of H and L chains allows the coexpression of two
RT mutually exclusive idiotopes (Id1104 and Id1558).";
RL J. Immunol. 146:4024-4030(1991).
DR EMBL; M74139; AAA37776.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON TER 1
SQ SEQUENCE 134 AA; 14908 MW; 1852D86D26FC7567 CRC64;

Query Match 71.3%; Score 423; DB 2; Length 134;
Best Local Similarity 70.9%; Pred. No. 9.3e-36;
Matches 83; Conservative 12; Mismatches 18; Indels 4; Gaps 1;
QY 1 EVOLVOSGAEEVPGASVKISCKASGSSFTGYNNMVRQNIKSLWIGALIDPYVGGTSY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 18 EVOLQSGPELVKPGASVKMSCKASGYTFDYMKVWKQSPGKSLWIGIDINPNNGTSY 77
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDVAVYCVSG---MEYWGQGTSTVTS 113
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 78 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVVYCARDYSYVFDYWGQGTTLTVSS 134
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 7
Q7TMK1 PRELIMINARY; PRT; 470 AA.
AC Q7TMK1;
DT 01-OCT-2003 (TEMBLrel. 25, Created)
DT 01-OCT-2003 (TEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Hypothetical protein A1324046.
GN Name=A1324046;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CZECH II; TISSUE=Mammary tumor;
RY MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Maman A., Rodriguez S., Sanchez A.,
RA Whiting M., Maman A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grummond J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RA Strausberg R.; to the EMBL/GenBank/DBJ databases.
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC055910; AAH55910.1; -.
DR HSSP; P01865; 1KB5.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR Hypothetical protein.
SQ SEQUENCE 470 AA; 51727 MW; 6D90E4DF896BB090 CRC64;

Query Match 70.2%; Score 416; DB 2; Length 470;
Best Local Similarity 69.4%; Pred. No. 2e-34;
Matches 84; Conservative 12; Mismatches 17; Indels 8; Gaps 2;
QY 1 EVOLVOSGAEEVPGASVKISCKASGSSFTGYNNMVRQNIKSLWIGALIDPYVGGTSY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 EVOLQSGPELVKPGASVKISCKASGYTFDYMKVWKQSHGKSLWIGLVNPNNGTSY 79
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDVAVYCV---SG---MEYWGQGTSTVTS 112
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 NQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVVYCYARYYSGSYWFDVWGAGTTVTS 139
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 113 S 113
Db 140 S 140

RESULT 8
Q91WR1 PRELIMINARY; PRT; 488 AA.
AC Q91WR1;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Igh-VJ558 protein.
GN Name=Igh-VJ558;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,	
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,	
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA	Villaion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA	Faney J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,	
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,	
RA	Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,	
RA	Jones S.J., Marra M.A.,	
RT	"Generation and initial analysis of more than 15,000 full-length human	
RT	and mouse cDNA sequences."	
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	
RL	[2]	
RN	SEQUENCE FROM N.A.	
RC	STRAIN=FVB/N; TISSUE=Kidney;	
RA	Strausberg R.;	
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; BC013539; AAH13539.1; -	
DR	HSP; P01751; IA6W.	
DR	MGI; 96486; Igh-VJ558.	
DR	Pfam; PF07654; Cl-set; 2.	
DR	SMART; SM00406; IGV; 1.	
DR	PROSITE; PS00835; IG_LIKE; 4.	
DR	PROSITE; PS00290; IG_MHC; UNKNOWN 2.	
SQ	SEQUENCE 488 AA; 52964 MW; F12068460B400B9D CRC64;	
	Query Match 70.1%; Score 415.5; DB 2; Length 488;	
	Best Local Similarity 65.3%; Pred. No. 2.3e-34;	
	Matches 81; Conservative 14; Mismatches 18; Indels 11; Gaps 1;	
QY	1 EVQLVQSGAEVKEPKGASVKISCKASGSGFTGYNNWVRQNIKGSLEWIGAIIDPYVGTSY 60	
Db	20 EVQLQSGPELVKPGASVKLSCKASGYTITDYYNWVKQSHGKSLIEWIDINPYNGTST 79	
QY	61 NQPKFGKRAITVDKSTSTAYMHLKSLTSETAVYVCVSGM-----EYWGQTSV 109	
Db	80 NQPKFKALITVDKSSIAIQLNLNLTSDSAVYICARGPVYYSFSDRGDYWGQGLV 139	
QY	110 TVSS 113	
Db	140 TVSA 143	
RESULT 9		
HV12_MOUSE		
ID	HV12_MOUSE STANDARD; PRT; 117 AA.	
AC	P01756;	
DT	21-JUL-1986 (Rel. 01, Created)	
DT	21-JUL-1986 (Rel. 01, Last sequence update)	
DT	05-JUL-2004 (Rel. 44, Last annotation update)	
DE	Ig heavy chain v region MOPC 104E.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.	
RX	MEDLINE=83075344; PubMed=6816276;	
RX	Kenry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,	
RA	Hood L.E.;	
RT	"Complete amino acid sequence of a mouse mu chain: homology among	
RT	heavy chain constant region domains.";	
RT	Biochemistry 21:5415-5424(1982).	
CC	-I- MISCELLANEOUS: The sequence of the light chain of this IgM myeloma	
CC	protein has also been determined.	
CC	-I- MISCELLANEOUS: This protein binds dextran.	
CC	-I- SIMILARITY: Contains 1 immunoglobulin-like domain.	
DR	PIR; A02039; MEMS4E.	

DR	PIR; PH1144; PH1144.
DR	PIR; PH1147; PH1147.
DR	PIR; PH1149; PH1149.
DR	PIR; PH1150; PH1150.
DR	PIR; PH1151; PH1151.
DR	PIR; PH1152; PH1152.
DR	PIR; PH1153; PH1153.
DR	HSP; P01751; IA6W.
DR	SMART; SM00406; IGV; 1.
DR	PROSITE; PS00835; IG_LIKE; 1.
FT	NON_TER 1 143
FT	NON_TER 143 143
SEQ	SEQUENCE 143 AA; 15868 MW; 139B2E96B81E07F CRC64;
Query Match	
Best Local Similarity 69.6%; Score 412.5; DB 2; Length 143;	
Matches 80; Conservative 12; Mismatches 21; Indels 5; Gaps 1	
Qy	1 EVQLVQSGAEVKEPGASVKISCKASGSSFTGYNNWVRQNIKGLKLEWIGALDIPYVGTSY 60
Db	1 QVQLQQPGAEVLKPGASVKLSCKASGYTFTSYNMHWYKQRPGRGLEWIGRIDPNSSGGTKY 60
Qy	61 NQPKFGKATLTVDKSTSTAYMHLKLSRSEDATVYCVS----GMVEYGGQTSVTVSS 113
Db	61 NERFKSKATLTVDRPSSATYMLQSLTSSEDSAVYICARWDEDYAMDYWGQTSVTVSS 118
RESULT 12	
HV13 MOUSE STANDARD; PRT; 117 AA.	
AC	P01757;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	05-JUL-2004 (Rel. 44, Last annotation update)
DE	Ig heavy chain V region J558.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RP	[1]
RP	SEQUENCE
RX	MEDLINE=00078170; PubMed=6765983;
RT	Schilling J., Clevinger B., Davies J.M., Hood L.;
RT	"Amino acid sequence of homogeneous antibodies to dextran and DNA
RT	rearrangements in heavy chain V-region gene segments.";
RL	Nature 283:35-40(1980).
CC	-1- MISCELLANEOUS: The sequences of 10 hybridoma proteins that also
CC	bind dextran differ from that shown at 1-7 positions, many of
CC	which occur in the D and J segments.
CC	-1- MISCELLANEOUS: This protein binds dextran.
CC	-1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR	PIR; A26242; MMSJ5.
DR	HSP; P01751; INQB.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003596; Ig_v.
DR	Pfam; PF00047; Ig; 1.
DR	SMART; SM00406; IGV; 1.
DR	PROSITE; PS00835; IG_LIKE; 1.
KW	Direct protein sequencing; Immunoglobulin V region.
FT	DOMAIN 1 116
FT	DISULFID 22 96
FT	NON_TER 117 117
SEQ	SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;
Query Match	
Best Local Similarity 69.5%; Score 412; DB 1; Length 117;	
Matches 82; Conservative 11; Mismatches 20; Indels 4; Gaps 1	
Qy	1 EVQLVQSGAEVKEPGASVKISCKASGSSFTGYNNWVRQNIKGLKLEWIGALDIPYVGTSY 60
Db	1 EVQLQQSGPELVKPGASVKRMSCKASGYTFTSYNMHWYKQSHGKLEWIGIDIPNNGTSY 60
Qy	61 NQPKFGKATLTVDKSTSTAYMHLKLSRSEDATVYCVS----MEYAGQGTSTVTVSS 113

DR EMBL; AB067789; BAB63274.1; --
DR PIR; F28833; F28833.
DR PIR; F33932; F33932.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR HSSP; P01751; 1A6W.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
FT NON_TER 1_1
SQ SEQUENCE 145 145

MM; 0162D0A26C746C04 CRC64;

Query Match 69.4%; Score 411.5; DB 2; Length 145;
Best Local Similarity 66.7%; Pred. No. 1.6e-34;
Matches 80; Conservative 12; Mismatches 21; Indels 7; Gaps 1;
QY 1 EVOLVSGAEVEKPGASVKISKASGSGTGYNNMNVRRNIGKSLWIGALDPYGGTSY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLQQPGAEVLKPGASVKLSKASGYTFTSYMMHWVKQRPGRGLEWIGRIDPNSGGTKY 60
QY 61 NQKFKRATLTVDKSTSTAYMHLKSLRSEDYVYCVS-----GMEYWGQTSVTYSS 113
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 NEKFKRATLTVDKPSSTAYMQLSLTSDSAVYICARYDGSFYAMDYWGQTSVTYSS 120

Search completed: April 18, 2005, 10:03:56
Job time : 85.5 secs

Result No.	Query			ID	Description	
	Score	Match	Length			
1	561	94.6	113	15	US-10-468-370-686	Sequence 686, App
2	561	94.6	113	16	US-10-468-496-2017	Sequence 2017, App
3	556	93.8	113	15	US-10-468-370-688	Sequence 688, App
4	556	93.8	113	16	US-10-468-496-2019	Sequence 2019, App
5	536	90.4	113	15	US-10-468-370-684	Sequence 684, App
6	536	90.4	113	16	US-10-468-496-2015	Sequence 2015, App
7	527	88.9	113	15	US-10-468-370-674	Sequence 674, App
8	527	88.9	113	16	US-10-468-496-2005	Sequence 2005, App
9	524	88.4	113	15	US-10-468-370-682	Sequence 682, App
10	524	88.4	113	16	US-10-468-496-2013	Sequence 2013, App
11	521	87.9	113	15	US-10-468-370-676	Sequence 676, App
12	521	87.9	113	16	US-10-468-496-2007	Sequence 2007, App
13	520	87.7	113	15	US-10-468-370-680	Sequence 680, App

```
Query Match          94.6%; Score 561; DB 15; Length 113;
Best Local Similarity 94.7%; Pred. No. 3.2e-44;
Matches 107; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EVLVQSGAEVKEPKGASVKISKAGSSFTGYNNMVRQNIKSLWIGAIIDPPYGGTSY 60
    |||||
DB 1 EVLVQSGEVEKPSASVKISKAGSSFTGYNNMVRQAIKSLWIGAIIDPPYGGTSY 60
    |||||

QY 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDATVYCVSGMEYWGQTSVTVSS 113
    |||||
DB 61 NQKFKGRATLTVDKSSSTAYMHLKSLTSDTAVYCVSGMEYWGQTTVTVSS 113
    |||||

RESULT 2
US-10-468-496-2017
; Sequence 2017, Application US/10468496
; Publication No. US20040180386A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
; TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED
; FILE REFERENCE: MER-117
; CURRENT APPLICATION NUMBER: US/10/468,496
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: 01105777.5
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 01106538.0
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01106536.4
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01107012.5
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 01106899.6
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 2036
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2017
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-496-2017

Query Match          94.6%; Score 561; DB 16; Length 113;
Best Local Similarity 94.7%; Pred. No. 3.2e-44;
Matches 107; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EVLVQSGAEVKEPKGASVKISKAGSSFTGYNNMVRQNIKSLWIGAIIDPPYGGTSY 60
    |||||
DB 1 EVLVQSGEVEKPSASVKISKAGSSFTGYNNMVRQAIKSLWIGAIIDPPYGGTSY 60
    |||||

QY 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDATVYCVSGMEYWGQTSVTVSS 113
    |||||
DB 61 NQKFKGRATLTVDKSSSTAYMHLKSLTSDTAVYCVSGMEYWGQTTVTVSS 113
    |||||

RESULT 3
US-10-468-370-688
; Sequence 688, Application US/10468370
; Publication No. US20040082039A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Carr, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Carter, Graham
```

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; APPLICANT: Hamilton, Anita
; APPLICANT: Williams, Stephen
; APPLICANT: Hanlon, Marian
; APPLICANT: Watkins, John
; APPLICANT: Baker, Matthew
; APPLICANT: Way, Jeffrey
; TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-118
; CURRENT APPLICATION NUMBER: US/10/468,370
; PRIOR FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: EP 01103955.9
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: EP 01108291.4
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: PCT/EP02/01690
; PRIOR FILING DATE: 2002-02-18
; NUMBER OF SEQ ID NOS: 689
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 688
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-468-370-688

Query Match          93.8%; Score 556; DB 15; Length 113;
Best Local Similarity 92.9%; Pred. No. 9.2e-44;
Matches 105; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 EVLVQSGAEVKEPKGASVKISKAGSSFTGYNNMVRQNIKSLWIGAIIDPPYGGTSY 60
    |||||
DB 1 EVLVQSGEVEKPSASVKISKAGSSFTGYNNMVRQNIKSLWIGAIIDPPYGGTSY 60
    |||||

QY 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDATVYCVSGMEYWGQTSVTVSS 113
    |||||
DB 61 NQKFKGRATLTVDKSSSTAYMHLKSLTSDTAVYCVSGMEYWGQTSVTVSS 113
    |||||

RESULT 4
US-10-468-496-2019
; Sequence 2019, Application US/10468496
; Publication No. US20040180386A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
; TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED
; FILE REFERENCE: MER-117
; CURRENT APPLICATION NUMBER: US/10/468,496
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: 01105777.5
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 01106538.0
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01106536.4
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01107012.5
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 01106899.6
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 2036
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2019
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-496-2019

Query Match          93.8%; Score 556; DB 16; Length 113;
Best Local Similarity 92.9%; Pred. No. 9.2e-44;
Matches 105; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 EVQLVSGAEVEKPGASVKISCKASGSSFTGYNNMWRQNIKSLRWIGALDPYVGTSY 60
Db 1 EVQLVSGAEVEKPGASVKISCKASGSSFTGYNNMWRQNIKSLRWIGALDPYVGTSY 60

QY 61 NQKFKGRATLTVDKSTAYMHLKSLRSEDATVYVCVSGMEYWGQTSVTSS 113
Db 61 NQKFKGRATLTVDKSSSTAYMHLKSLTSDSAVYVCVSGMEYWGQTSVTSS 113

RESULT 5
US-10-468-370-684
; Sequence 684, Application US/10468370
; Publication No. US20040082039A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Carr, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Carter, Graham
; APPLICANT: Hamilton, Anita
; APPLICANT: Williams, Stephen
; APPLICANT: Hanlon, Marian
; APPLICANT: Watkins, John
; APPLICANT: Baker, Matthew
; APPLICANT: Way, Jeffrey
; TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
; FILE REFERENCE: MER-118
; CURRENT APPLICATION NUMBER: US/10/468,370
; PRIOR FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: EP 01103955.9
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: EP 01108291.4
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: PCT/EP02/01690
; PRIOR FILING DATE: 2002-02-18
; NUMBER OF SEQ ID NOS: 689
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 684
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: De-immunized MHC class II binding epitope
US-10-468-370-684

Query Match          90.4%; Score 536; DB 15; Length 113;
Best Local Similarity 88.5%; Pred. No. 6.4e-42;
Matches 100; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 EVQLVSGAEVEKPGASVKISCKASGSSFTGYNNMWRQNIKSLRWIGALDPYVGTSY 60
Db 1 EVQLVSGAEVEKPGASVKISCKASGSSFTGYNNMWRQNIKSLRWIGALDPYVGTSY 60

QY 61 NQKFKGRATLTVDKSTAYMHLKSLRSEDATVYVCVSGMEYWGQTSVTSS 113
Db 61 NQKFKGRVTITVDKSSQAYMHLKSLTSDATVYVCVSGMEYWGQTTVTSS 113

RESULT 6
US-10-468-496-2015
; Sequence 2015, Application US/10468496
; Publication No. US20040180386A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; APPLICANT: Gillies, Stephen
; APPLICANT: Carr, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Carter, Graham
; APPLICANT: Hamilton, Anita
; APPLICANT: Williams, Stephen
; APPLICANT: Hanlon, Marian
; APPLICANT: Watkins, John
; APPLICANT: Baker, Matthew
; APPLICANT: Way, Jeffrey
; TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
; FILE REFERENCE: MER-118
; CURRENT APPLICATION NUMBER: US/10/468,370
; PRIOR FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: EP 01103955.9
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: EP 01108291.4
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: PCT/EP02/01690
; PRIOR FILING DATE: 2002-02-18
; NUMBER OF SEQ ID NOS: 689
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 684
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: De-immunized MHC class II binding epitope
US-10-468-370-674
; Sequence 674, Application US/10468370
; Publication No. US20040082039A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Carr, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Carter, Graham
; APPLICANT: Hamilton, Anita
; APPLICANT: Williams, Stephen
; APPLICANT: Hanlon, Marian
; APPLICANT: Watkins, John
; APPLICANT: Baker, Matthew
; APPLICANT: Way, Jeffrey
; TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
; FILE REFERENCE: MER-118
; CURRENT APPLICATION NUMBER: US/10/468,370
; PRIOR FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: EP 01103955.9
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: EP 01108291.4
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: PCT/EP02/01690
; PRIOR FILING DATE: 2002-02-18
; NUMBER OF SEQ ID NOS: 689
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 674
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-496-2015

Query Match          90.4%; Score 536; DB 16; Length 113;
Best Local Similarity 88.5%; Pred. No. 6.4e-42;
Matches 100; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 EVQLVSGAEVEKPGASVKISCKASGSSFTGYNNMWRQNIKSLRWIGALDPYVGTSY 60
Db 1 EVQLVSGAEVEKPGASVKISCKASGSSFTGYNNMWRQNIKSLRWIGALDPYVGTSY 60

QY 61 NQKFKGRATLTVDKSTAYMHLKSLRSEDATVYVCVSGMEYWGQTSVTSS 113
Db 61 NQKFKGRVTITVDKSSQAYMHLKSLTSDATVYVCVSGMEYWGQTTVTSS 113

RESULT 7
US-10-468-370-674
; Sequence 674, Application US/10468370
; Publication No. US20040082039A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Carr, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Carter, Graham
; APPLICANT: Hamilton, Anita
; APPLICANT: Williams, Stephen
; APPLICANT: Hanlon, Marian
; APPLICANT: Watkins, John
; APPLICANT: Baker, Matthew
; APPLICANT: Way, Jeffrey
; TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
; FILE REFERENCE: MER-118
; CURRENT APPLICATION NUMBER: US/10/468,370
; PRIOR FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: EP 01103955.9
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: EP 01108291.4
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: PCT/EP02/01690
; PRIOR FILING DATE: 2002-02-18
; NUMBER OF SEQ ID NOS: 689
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 674
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-496-2015
```

```
/ TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-370-674

Query Match      88.9%; Score 527; DB 15; Length 113;
Best Local Similarity 87.6%; Pred. No. 4.3e-41;
Matches 99; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 EVLVQSGAEVEKPGASVKISCKASGSSFTGNNMNRQNIKSLWIGALDPYGGTSY 60
Db 1 EVQLLQSGPELKPGASVKISCKASGSSFTGNNMNRQAPQGLWIGALDPYGGTSY 60

QY 61 NQKFKGRATLTVDKSTAYMHLKSLRSEDATVYVCVSGMEYWGQTSVTVSS 113
Db 61 NQKFKGRATLSVDKSSQAYMHLKSLTSDSAVYVCVSGMEYWGQTTVTVSS 113

RESULT 8
US-10-468-496-2005
; Sequence 2005, Application US/10468496
; Publication No. US20040180386A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
; TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED
; FILE REFERENCE: MER-117
; CURRENT APPLICATION NUMBER: US/10/468,496
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: 01105777.5
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 01107012.5
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 01106899.6
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 2036
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2005
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-496-2005

Query Match      88.9%; Score 527; DB 16; Length 113;
Best Local Similarity 87.6%; Pred. No. 4.3e-41;
Matches 99; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 EVLVQSGAEVEKPGASVKISCKASGSSFTGNNMNRQNIKSLWIGALDPYGGTSY 60
Db 1 EVQLLQSGPELKPGASVKISCKASGSSFTGNNMNRQAPQGLWIGALDPYGGTSY 60

QY 61 NQKFKGRATLTVDKSTAYMHLKSLRSEDATVYVCVSGMEYWGQTSVTVSS 113
Db 61 NQKFKGRATLSVDKSSQAYMHLKSLTSDSAVYVCVSGMEYWGQTTVTVSS 113

RESULT 9
US-10-468-370-682
; Sequence 682, Application US/10468370
; Publication No. US20040082039A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Carr, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Carter, Graham
; APPLICANT: Hamilton, Anita
; APPLICANT: Williams, Stephen
; APPLICANT: Hanlon, Marian
; APPLICANT: Watkins, John
; APPLICANT: Baker, Matthew
; APPLICANT: Way, Jeffrey
; TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-118
; CURRENT APPLICATION NUMBER: US/10/468,370
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: EP 01103955.9
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: EP 01108291.4
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: PCT/EP02/01690
; PRIOR FILING DATE: 2002-02-18
; NUMBER OF SEQ ID NOS: 689
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 682
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: De-immunized MHC class II binding epitope
US-10-468-370-682

Query Match      88.4%; Score 524; DB 15; Length 113;
Best Local Similarity 86.7%; Pred. No. 8.2e-41;
Matches 98; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 EVLVQSGAEVEKPGASVKISCKASGSSFTGNNMNRQNIKSLWIGALDPYGGTSY 60
Db 1 EVQLLQSGPELKPGASVKISCKASGSSFTGNNMNRQAPQGLWIGALDPYGGTSY 60

QY 61 NQKFKGRATLTVDKSTAYMHLKSLRSEDATVYVCVSGMEYWGQTSVTVSS 113
Db 61 NQKFKGRVTITVDKSSQAYMHLKSLTSDATVYVCVSGMEYWGQTTVTVSS 113

RESULT 10
US-10-468-496-2013
; Sequence 2013, Application US/10468496
; Publication No. US20040180386A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
; TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED
; FILE REFERENCE: MER-117
; CURRENT APPLICATION NUMBER: US/10/468,496
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: 01105777.5
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 01106538.0
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01106536.4
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01107012.5
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 01106899.6
```



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/ PRIOR FILING DATE: 2001-03-20
/ NUMBER OF SEQ ID NOS: 2036
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2013
/ LENGTH: 113
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: MHC class II binding epitope
US-10-468-496-2013

Query Match      88.4%; Score 524; DB 16; Length 113;
Best Local Similarity 86.7%; Pred. No. 8.2e-41;
Matches 98; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 EVLVQSGAEVEKPGASVKISCKASGSSFTGYNNMNVQRNIGKSLWIGALDPYGGTSY 60
Db 1 EVLVQSGPELKPGASVKISCKASGSSFTGYNNMNVQRNIGKSLWIGALDPYGGTSY 60

QY 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDVAVYCVSGMEYWGQTSVTVSS 113
Db 61 NQKFKGRVTITADKSSQAYMHLKSLTSEDVAVYCVSGMEYWGQTTVTVSS 113

RESULT 11
US-10-468-370-676
/ Sequence 676, Application US/10468370
/ Publication No. US20040082039A1
/ GENERAL INFORMATION:
/ APPLICANT: Gillies, Stephen
/ APPLICANT: Carr, Francis J.
/ APPLICANT: Jones, Tim
/ APPLICANT: Carter, Graham
/ APPLICANT: Hamilton, Anita
/ APPLICANT: Williams, Stephen
/ APPLICANT: Hanlon, Marian
/ APPLICANT: Watkins, John
/ APPLICANT: Baker, Matthew
/ APPLICANT: Way, Jeffrey
/ TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
/ TITLE OF INVENTION: IMMUNOGENICITY
/ FILE REFERENCE: MER-118
/ CURRENT APPLICATION NUMBER: US/10/468,370
/ PRIOR FILING DATE: 2003-08-19
/ PRIOR APPLICATION NUMBER: EP 01103955.9
/ PRIOR FILING DATE: 2001-02-19
/ PRIOR APPLICATION NUMBER: EP 01108291.4
/ PRIOR FILING DATE: 2001-04-05
/ PRIOR APPLICATION NUMBER: PCT/EP02/01690
/ PRIOR FILING DATE: 2002-02-18
/ NUMBER OF SEQ ID NOS: 689
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 676
/ LENGTH: 113
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: De-immunized MHC class II binding epitope
US-10-468-370-676

Query Match      87.9%; Score 521; DB 15; Length 113;
Best Local Similarity 85.8%; Pred. No. 1.6e-40;
Matches 97; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 EVLVQSGAEVEKPGASVKISCKASGSSFTGYNNMNVQRNIGKSLWIGALDPYGGTSY 60
Db 1 EVLVQSGPELKPGASVKISCKASGSSFTGYNNMNVQRNIGKSLWIGALDPYGGTSY 60

QY 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDVAVYCVSGMEYWGQTSVTVSS 113
Db 61 NQKFKSRVTITADKSSQAYMHLKSLTSEDVAVYCVSGMEYWGQTTVTVSS 113

RESULT 12
US-10-468-496-2007
/ Sequence 2007, Application US/10468496
/ Publication No. US20040180386A1
/ GENERAL INFORMATION:
/ APPLICANT: Carr, Francis J.
/ APPLICANT: Carter, Graham
/ APPLICANT: Jones, Tim
/ APPLICANT: Williams, Stephen
/ APPLICANT: Hamilton, Anita
/ TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
/ TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED
/ TITLE OF INVENTION: IMMUNOGENICITY
/ FILE REFERENCE: MER-117
/ CURRENT APPLICATION NUMBER: US/10/468,496
/ PRIOR FILING DATE: 2003-09-25
/ PRIOR APPLICATION NUMBER: 01103954.2
/ PRIOR FILING DATE: 2001-02-19
/ PRIOR APPLICATION NUMBER: 01105777.5
/ PRIOR FILING DATE: 2001-03-08
/ PRIOR APPLICATION NUMBER: 01106538.0
/ PRIOR FILING DATE: 2001-03-15
/ PRIOR APPLICATION NUMBER: 01106536.4
/ PRIOR FILING DATE: 2001-03-15
/ PRIOR APPLICATION NUMBER: 01107012.5
/ PRIOR FILING DATE: 2001-03-20
/ PRIOR APPLICATION NUMBER: 01106899.6
/ PRIOR FILING DATE: 2001-03-20
/ NUMBER OF SEQ ID NOS: 2036
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2007
/ LENGTH: 113
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: MHC class II binding epitope
US-10-468-496-2007

Query Match      87.9%; Score 521; DB 16; Length 113;
Best Local Similarity 85.8%; Pred. No. 1.6e-40;
Matches 97; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 EVLVQSGAEVEKPGASVKISCKASGSSFTGYNNMNVQRNIGKSLWIGALDPYGGTSY 60
Db 1 EVLVQSGPELKPGASVKISCKASGSSFTGYNNMNVQRNIGKSLWIGALDPYGGTSY 60

QY 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDVAVYCVSGMEYWGQTSVTVSS 113
Db 61 NQKFKSRVTITADKSSQAYMHLKSLTSEDVAVYCVSGMEYWGQTTVTVSS 113

RESULT 13
US-10-468-370-680
/ Sequence 680, Application US/10468370
/ Publication No. US20040082039A1
/ GENERAL INFORMATION:
/ APPLICANT: Gillies, Stephen
/ APPLICANT: Carr, Francis J.
/ APPLICANT: Jones, Tim
/ APPLICANT: Carter, Graham
/ APPLICANT: Hamilton, Anita
/ APPLICANT: Williams, Stephen
/ APPLICANT: Hanlon, Marian
/ APPLICANT: Watkins, John
/ APPLICANT: Baker, Matthew
/ APPLICANT: Way, Jeffrey
/ TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
/ TITLE OF INVENTION: IMMUNOGENICITY
/ FILE REFERENCE: MER-118
/ CURRENT APPLICATION NUMBER: US/10/468,370
/ PRIOR FILING DATE: 2003-08-19
/ PRIOR APPLICATION NUMBER: EP 01103955.9
/ PRIOR FILING DATE: 2001-02-19
```

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; PRIOR APPLICATION NUMBER: EP 01108291.4
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: PCT/EP02/01690
; PRIOR FILING DATE: 2002-02-18
; NUMBER OF SEQ ID NOS: 689
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 680
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: De-immunized MHC class II binding epitope
US-10-468-370-680

Query Match      87.7%; Score 520; DB 15; Length 113;
Best Local Similarity 85.8%; Pred. No. 1.9e-40;
Matches 97; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 EVQLVSGAEVEKPGASVKISCKASGSSFTGYNNMVRQNIKSLWIGAIDPYGGSY 60
Db 1 EVQLVSGAEVEKPGASVKISCKASGSSFTGYNNMVRQNIKSLWIGAIDPYGGSY 60

QY 61 NQKFKGRATLVDKSTSTAYMHLKSLRSEDVAVYCVSGMEYWGQTSVTSS 113
Db 61 NQKFKGRVTITADKSSQAYMHLKSLTSEDVAVYCVSGMEYWGQTSVTSS 113

RESULT 14
US-10-468-496-2011
; Sequence 2011, Application US/10468496
; Publication No. US20040180386A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
; TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED
; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-117
; CURRENT APPLICATION NUMBER: US/10/468,496
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: 01105777.5
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 01106538.0
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01106536.4
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01107012.5
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 01106899.6
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 2036
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2011
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-496-2011
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Query Match      87.7%; Score 520; DB 16; Length 113;
Best Local Similarity 85.8%; Pred. No. 1.9e-40;
Matches 97; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 EVQLVSGAEVEKPGASVKISCKASGSSFTGYNNMVRQNIKSLWIGAIDPYGGSY 60
Db 1 EVQLVSGAEVEKPGASVKISCKASGSSFTGYNNMVRQNIKSLWIGAIDPYGGSY 60
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QY 61 NQKFKGRATLVDKSTSTAYMHLKSLRSEDVAVYCVSGMEYWGQTSVTSS 113
Db 61 NQKFKGRVTITADKSSQAYMHLKSLTSEDVAVYCVSGMEYWGQTSVTSS 113

RESULT 15
US-10-468-370-678
; Sequence 678, Application US/10468370
; Publication No. US20040082039A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Carr, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Carter, Graham
; APPLICANT: Hamilton, Anita
; APPLICANT: Williams, Stephen
; APPLICANT: Hanlon, Marian
; APPLICANT: Watkins, John
; APPLICANT: Baker, Matthew
; APPLICANT: Way, Jeffrey
; TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-118
; CURRENT APPLICATION NUMBER: US/10/468,370
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: EP 01103955.9
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: EP 01108291.4
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: PCT/EP02/01690
; PRIOR FILING DATE: 2002-02-18
; NUMBER OF SEQ ID NOS: 689
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 678
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: De-immunized MHC class II binding epitope
US-10-468-370-678

Query Match      86.7%; Score 514; DB 15; Length 113;
Best Local Similarity 85.0%; Pred. No. 6.9e-40;
Matches 96; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 1 EVQLVSGAEVEKPGASVKISCKASGSSFTGYNNMVRQNIKSLWIGAIDPYGGSY 60
Db 1 EVQLVSGAEVEKPGASVKISCKASGSSFTGYNNMVRQNIKSLWIGAIDPYGGSY 60

QY 61 NQKFKGRATLVDKSTSTAYMHLKSLRSEDVAVYCVSGMEYWGQTSVTSS 113
Db 61 NQKFKGRVTITADKSSQAYMHLKSLTSEDVAVYCVSGMEYWGQTSVTSS 113

Search completed: April 18, 2005, 10:17:26
Job time : 70 secs
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OM protein - protein search, using sw model

Run on: April 18, 2005, 09:57:36 ; Search time 19 Seconds
(without alignments)
443.965 Million cell updates/sec

Title: US-10-737-208A-2

Perfect score: 593

Sequence: 1 EVQLVQSGAEVEKPGASVKI.....YYCVSGMEYWGQTSVTSS 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/prodata/1/iaa/5A COMB.pep:*

2: /cgn2_6/prodata/1/iaa/5B COMB.pep:*

3: /cgn2_6/prodata/1/iaa/6A COMB.pep:*

4: /cgn2_6/prodata/1/iaa/6B COMB.pep:*

5: /cgn2_6/prodata/1/iaa/6C COMB.pep:*

6: /cgn2_6/prodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	473.5	79.8	120	2	US-08-002-324-2
2	473.5	79.8	120	5	PCT-US94-00261-2
3	464	78.2	130	4	US-09-556-605-3
4	458	77.2	267	4	US-09-419-788-30
5	453	76.4	117	3	US-08-525-539A-78
6	453	76.4	136	3	US-08-525-539A-63
7	451.5	76.1	118	4	US-09-647-468-139
8	451.5	76.1	118	4	US-09-647-468-140
9	451.5	76.1	137	4	US-09-647-468-153
10	451.5	76.1	137	4	US-09-647-468-154
11	449.5	75.8	297	4	US-09-486-814A-2
12	447.5	75.5	116	2	US-08-273-146-55
13	447.5	75.5	133	3	US-08-718-323A-8
14	447.5	75.5	133	4	US-09-587-526-8
15	445.5	75.1	116	1	US-07-634-278-57
16	445.5	75.1	116	1	US-07-634-278-73
17	445.5	75.1	116	1	US-08-477-728-57
18	445.5	75.1	116	1	US-08-477-728-73
19	445.5	75.1	116	1	US-08-474-040-57
20	445.5	75.1	116	1	US-08-474-040-73
21	445.5	75.1	116	1	US-08-487-200-57
22	445.5	75.1	116	1	US-08-487-200-73
23	445.5	75.1	116	3	US-08-484-537-57
24	445.5	75.1	116	3	US-08-484-537-73
25	445.5	75.1	135	1	US-08-137-117D-27
26	445.5	75.1	135	1	US-08-137-117D-102
27	445.5	75.1	135	2	US-08-436-717-27

28	445.5	75.1	135	2	US-08-436-717-102	Sequence 102, Appl
29	445	75.0	241	4	US-09-581-345-5	Sequence 5, Appl
30	444.5	75.0	116	2	US-08-561-521-41	Sequence 41, Appl
31	444.5	75.0	116	5	PCT-US95-01219-41	Sequence 41, Appl
32	444	74.9	111	3	US-08-881-037-20	Sequence 20, Appl
33	442.5	74.6	135	1	US-08-137-117D-112	Sequence 112, Appl
34	442.5	74.6	135	2	US-08-436-717-112	Sequence 112, Appl
35	441.5	74.5	116	1	US-07-634-278-56	Sequence 56, Appl
36	441.5	74.5	116	1	US-08-477-728-56	Sequence 56, Appl
37	441.5	74.5	116	1	US-08-474-040-56	Sequence 56, Appl
38	441.5	74.5	116	1	US-08-487-200-56	Sequence 56, Appl
39	441.5	74.5	116	3	US-08-484-537-56	Sequence 56, Appl
40	441.5	74.5	135	1	US-07-634-278-69	Sequence 69, Appl
41	441.5	74.5	135	1	US-08-477-728-69	Sequence 69, Appl
42	441.5	74.5	135	1	US-08-474-040-69	Sequence 69, Appl
43	441.5	74.5	135	1	US-08-487-200-69	Sequence 69, Appl
44	441.5	74.5	135	3	US-08-484-537-69	Sequence 69, Appl
45	440	74.2	119	4	US-09-232-290-37	Sequence 37, Appl

ALIGNMENTS

RESULT 1
US-08-002-324-2
; Sequence 2, Application US/08002324
; Patent No. 5861156
; GENERAL INFORMATION:
; APPLICANT: George, Andrew J.T.
; APPLICANT: Segal, David M.
; APPLICANT: Huston, James S.
; TITLE OF INVENTION: METHODS OF DELIVERING AGENTS TO TARGET
; TITLE OF INVENTION: CELLS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS: 20
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/002,324
; FILING DATE: 19930108
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CEM92-02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 981-6240
; TELEFAX: (617) 981-9540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-002-324-2

Query Match 79.8%; Score 473.5; DB 2; Length 120;
Best Local Similarity 75.0%; Pred. No. 2.6e-40;
Matches 90; Conservative 13; Mismatches 10; Indels 7; Gaps 1;
QY 1 EVQLVQSGAEVEKPGASVKISCKASGSSPTGYNMHWVRONICKSLEWIGAIPIYGGTSY 60
DB 1 QVQLQSGPELEKPGASVKISCKASGYSPTGIMNWKQNGKSLWIGNIAPYYGGTSY 60

QY 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDATVYVC-----VSGMEYWGQTSVTVSS 113
Db 61 NQKFKGRATLTVDKSSSTAYMQLSSTLSDSAVYFCARWGGTMITGLDWGQGTTLTVSS 120

RESULT 2

PCT-US94-00261-2
; Sequence 2, Application PC/TUS9400261
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT: 1
; TITLE OF INVENTION: METHODS OF DELIVERING AGENTS TO
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/00261
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CBM92-02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 981-6240
; TELEFAX: (617) 981-9540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-00261-2

Query Match 79.8%; Score 473.5; DB 5; Length 120;
Best Local Similarity 75.0%; Pred. No. 2.6e-40;
Matches 90; Conservative 13; Mismatches 10; Indels 7; Gaps 1;

QY 1 EVOLVSGAEVKEPKGASVKISKAGSSFTGYNNMNVQRNIGKSLWIGAIIDPYYGTSY 60
Db 1 QVQLQSGPELEKPKGASVKISKAGSYFTGYIMNVKQNNKSLWIGNIAPYYGTSY 60
QY 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDATVYVC-----VSGMEYWGQTSVTVSS 113
Db 61 NQKFKGRATLTVDKSSSTAYMQLSSTLSDSAVYFCARWGGTMITGLDWGQGTTLTVSS 120

RESULT 3

US-09-556-605-3
; Sequence 3, Application US/09556605
; Patent No. 6417324
; GENERAL INFORMATION:
; APPLICANT: Sallberg, Matti
; APPLICANT: Lardina, Una
; TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE
; FILE REFERENCE: HEPATITIS B VIRUS CORE AND E ANTIGENS
; FILE REFERENCE: TRIPEP.020A
; CURRENT APPLICATION NUMBER: US/09/556,605
; CURRENT FILING DATE: 2000-04-21
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 130

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Oligonucleotide
US-09-556-605-3

Query Match 78.2%; Score 464; DB 4; Length 130;
Best Local Similarity 76.7%; Pred. No. 2.6e-39;
Matches 89; Conservative 10; Mismatches 13; Indels 4; Gaps 1;
QY 2 VOLVQSGAEVKEPKGASVKISKAGSSFTGYNNMNVQRNIGKSLWIGAIIDPYYGTSY 61
Db 1 IQLQSGAEVKEPKGASVKISKAGSYFTGYNNMNVKQSHGKSLWIGNINPYYGTSY 60
QY 62 QKFKGRATLTVDKSTSTAYMHLKSLRSEDATVYVC-----SGMEYWGQTSVTVSS 113
Db 61 QKFKGRATLTVDKSSSTAYMQLSSTLSDSAVYFCARGKGTGTFAYWGQGTTLTVSSA 116

RESULT 4

US-09-419-788-30
; Sequence 30, Application US/09419788
; Patent No. 6825325
; GENERAL INFORMATION:
; APPLICANT: FISCHER, Rainer
; APPLICANT: SCHILLBERG, Stefan
; APPLICANT: NAHRING, Jorg
; APPLICANT: SACK, Markus
; APPLICANT: MONECKE, Michael
; APPLICANT: LIAO, Yu-Cai
; APPLICANT: SPIEGEL, Holger
; APPLICANT: ZIMMERMAN, Sabine
; APPLICANT: EMANS, Neil
; TITLE OF INVENTION: Molecular Pathogenicide Mediated Plant Disease
; FILE REFERENCE: 0147-0189P
; CURRENT APPLICATION NUMBER: US/09/419,788
; CURRENT FILING DATE: 1999-10-18
; EARLIER APPLICATION NUMBER: 98 11 9630.6 EP
; EARLIER FILING DATE: 1998-10-16
; EARLIER APPLICATION NUMBER: 66/BOM/1998 INDIA
; EARLIER FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 30
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic, no
; OTHER INFORMATION: natural origin
US-09-419-788-30

Query Match 77.2%; Score 458; DB 4; Length 267;
Best Local Similarity 75.6%; Pred. No. 2.4e-38;
Matches 90; Conservative 8; Mismatches 15; Indels 6; Gaps 1;
QY 1 EVOLVQSGAEVKEPKGASVKISKAGSSFTGYNNMNVQRNIGKSLWIGAIIDPYYGTSY 60
Db 1 EVKLQSGAEVKEPKGASVKISKAGSYFTGYNNMNVKQSHGKSLWIGNINPYYGTSY 60
QY 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDATVYVCVG-----MEYWGQTSVTVSS 113
Db 61 NQKFKGRATLTVDKSSSTAYMQLSSTLSDSAVYFCARGVVDVDFAYWGQGTTLTVSS 119

RESULT 5

US-08-525-539A-78
; Sequence 78, Application US/08525539A
; Patent No. 6309636
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.R.
; APPLICANT: CERIANI, ROBERTO L.

APPLICANT: PETERSON, JERRY A.
TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,539A
FILING DATE: 14-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DYLAN, TYLER
REGISTRATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 27633-20001.21
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141

INFORMATION FOR SEQ ID NO: 78:

SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-525-539A-78

Query Match 76.4%; Score 453; DB 3; Length 117;
Best Local Similarity 75.2%; Pred. No. 2.9e-38;
Matches 88; Conservative 11; Mismatches 14; Indels 4; Gaps 1;

QY 1 EVQLVQSGAEVKPGASVKISCKASGSSFTGYNNMVRQNIKSLWIGALDIPYGGTSY 60
DB 1 EVQLVQSGAEVKPGASVKISCKASGSSFTGYNNMVRQNIKSLWIGALDIPYGGTSY 60
QY 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDATVYFCARRWRYTMDYWGQGLTVTVSS 113
DB 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDATVYFCARRWRYTMDYWGQGLTVTVSS 117

RESULT 6
US-08-525-539A-63
Sequence 63, Application US/08525539A
Patent No. 6309636
GENERAL INFORMATION:
APPLICANT: DO COUTO, FERNANDO J.R.
APPLICANT: CERIANI, ROBERTO L.
APPLICANT: PETERSON, JERRY A.
TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent in Release #1.0, Version #1.30

SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,539A
FILING DATE: 14-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DYLAN, TYLER
REGISTRATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 27633-20001.21
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141

INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 136 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-525-539A-63

Query Match 76.4%; Score 453; DB 3; Length 136;
Best Local Similarity 75.2%; Pred. No. 3.5e-38;
Matches 88; Conservative 11; Mismatches 14; Indels 4; Gaps 1;

QY 1 EVQLVQSGAEVKPGASVKISCKASGSSFTGYNNMVRQNIKSLWIGALDIPYGGTSY 60
DB 20 EVQLVQSGAEVKPGASVKISCKASGSSFTGYNNMVRQNIKSLWIGALDIPYGGTSY 79
QY 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDATVYFCARRWRYTMDYWGQGLTVTVSS 113
DB 80 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDATVYFCARRWRYTMDYWGQGLTVTVSS 136

RESULT 7
US-09-647-468-139
Sequence 139, Application US/09647468
Patent No. 6677436
GENERAL INFORMATION:
APPLICANT: SATO, KOH
APPLICANT: ADACHI, HIDEKI
APPLICANT: YABUTA, NAOKI
TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
FILE REFERENCE: 053466/0289
CURRENT APPLICATION NUMBER: US/09/647,468
CURRENT FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: PCT/JP99/01768
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: JP 10-91850
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 183
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 139
LENGTH: 118
TYPE: PRT
ORGANISM: Mus sp.
FEATURE:
OTHER INFORMATION: Amino acid sequence of H chain V region of anti-TF
OTHER INFORMATION: mouse monoclonal antibody ATR-2
US-09-647-468-139

Query Match 76.1%; Score 451.5; DB 4; Length 118;
Best Local Similarity 72.9%; Pred. No. 4.2e-38;
Matches 86; Conservative 12; Mismatches 15; Indels 5; Gaps 1;

QY 1 EVQLVQSGAEVKPGASVKISCKASGSSFTGYNNMVRQNIKSLWIGALDIPYGGTSY 60
DB 1 EVQLVQSGAEVKPGASVKISCKASGSSFTGYNNMVRQNIKSLWIGALDIPYGGTSY 60
QY 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDATVYFCARRWRYTMDYWGQGLTVTVSS 113
DB 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDATVYFCARRWRYTMDYWGQGLTVTVSS 118

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RESULT 8
US-09-647-468-140
; Sequence 140, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUTA, NAHIO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 140
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of H chain V region of anti-TF
; OTHER INFORMATION: mouse monoclonal antibody ATR-3
US-09-647-468-140

Query Match          76.1%; Score 451.5; DB 4; Length 118;
Best Local Similarity 72.9%; Pred. No. 4.2e-38;
Matches 86; Conservative 12; Mismatches 15; Indels 5; Gaps 1;

QY 1 EVLVQSGAEVEKPGASVKISKASGSGFTGYNMWRQNIKSLWIGALDPYGGTYSY 60
DB 1 EIQLQSGPELVKPGASVKISKASGSGFTDYNMWRQNIKSLWIGALDPYGGTII 60
QY 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDPAVYCVSG-----MEYWGQGTSTVSS 113
DB 61 NQKFKGRATLTVDKSSSTAFMHLNSLTSEDSAVYCVARGEGYFDYWGQGTTLTVSS 118

RESULT 9
US-09-647-468-153
; Sequence 153, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUTA, NAHIO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 153
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence coding for H chain V region of ant-TF
; OTHER INFORMATION: mouse monoclonal antibody ATR-2
US-09-647-468-153

Query Match          76.1%; Score 451.5; DB 4; Length 137;
Best Local Similarity 72.9%; Pred. No. 4.2e-38;
Matches 86; Conservative 12; Mismatches 15; Indels 5; Gaps 1;

QY 1 EVLVQSGAEVEKPGASVKISKASGSGFTGYNMWRQNIKSLWIGALDPYGGTYSY 60
DB 1 EIQLQSGPELVKPGASVKISKASGSGFTDYNMWRQNIKSLWIGALDPYGGTII 60
QY 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDPAVYCVSG-----MEYWGQGTSTVSS 113
DB 61 NQKFKGRATLTVDKSSSTAFMHLNSLTSEDSAVYCVARGEGYFDYWGQGTTLTVSS 118

RESULT 10
US-09-647-468-154
; Sequence 154, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUTA, NAHIO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 154
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence coding for H chain V region of ant-TF
; OTHER INFORMATION: mouse monoclonal antibody ATR-3
US-09-647-468-154

Query Match          76.1%; Score 451.5; DB 4; Length 137;
Best Local Similarity 72.9%; Pred. No. 5e-38;
Matches 86; Conservative 12; Mismatches 15; Indels 5; Gaps 1;

QY 1 EVLVQSGAEVEKPGASVKISKASGSGFTGYNMWRQNIKSLWIGALDPYGGTYSY 60
DB 20 EIQLQSGPELVKPGASVKISKASGSGFTDYNMWRQNIKSLWIGALDPYGGTII 79
QY 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDPAVYCVSG-----MEYWGQGTSTVSS 113
DB 80 NQKFKGRATLTVDKSSSTAFMHLNSLTSEDSAVYCVARGEGYFDYWGQGTTLTVSS 137

RESULT 11
US-09-486-814A-2
; Sequence 2, Application US/09486814A
; Patent No. 6562599
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, Masato
; APPLICANT: HAYASHI, No. 6562599io
; APPLICANT: YAMAMOTO, Hiroko
; APPLICANT: TOHDOH, Naoki
; TITLE OF INVENTION: SINGLE-CHAIN ANTIBODY AGAINST HEPATITIS B VIRUS CORE
; TITLE OF INVENTION: PROTEIN, GENE THEREOF, AND THERAPEUTIC AGENT FOR
; TITLE OF INVENTION: HEPATITIS B CONTAINING THESE
; FILE REFERENCE: 0020-4682P
; CURRENT APPLICATION NUMBER: US/09/486,814A
; CURRENT FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 297

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Best Local Similarity 72.9%; Pred. No. 5e-38;
Matches 86; Conservative 12; Mismatches 15; Indels 5; Gaps 1;

QY 1 EVLVQSGAEVEKPGASVKISKASGSGFTGYNMWRQNIKSLWIGALDPYGGTYSY 60
DB 20 EIQLQSGPELVKPGASVKISKASGSGFTDYNMWRQNIKSLWIGALDPYGGTII 79
QY 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDPAVYCVSG-----MEYWGQGTSTVSS 113
DB 80 NQKFKGRATLTVDKSSSTAFMHLNSLTSEDSAVYCVARGEGYFDYWGQGTTLTVSS 137

RESULT 10
US-09-647-468-154
; Sequence 154, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUTA, NAHIO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 154
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence coding for H chain V region of ant-TF
; OTHER INFORMATION: mouse monoclonal antibody ATR-3
US-09-647-468-154

Query Match          76.1%; Score 451.5; DB 4; Length 137;
Best Local Similarity 72.9%; Pred. No. 5e-38;
Matches 86; Conservative 12; Mismatches 15; Indels 5; Gaps 1;

QY 1 EVLVQSGAEVEKPGASVKISKASGSGFTGYNMWRQNIKSLWIGALDPYGGTYSY 60
DB 20 EIQLQSGPELVKPGASVKISKASGSGFTDYNMWRQNIKSLWIGALDPYGGTII 79
QY 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDPAVYCVSG-----MEYWGQGTSTVSS 113
DB 80 NQKFKGRATLTVDKSSSTAFMHLNSLTSEDSAVYCVARGEGYFDYWGQGTTLTVSS 137

RESULT 11
US-09-486-814A-2
; Sequence 2, Application US/09486814A
; Patent No. 6562599
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, Masato
; APPLICANT: HAYASHI, No. 6562599io
; APPLICANT: YAMAMOTO, Hiroko
; APPLICANT: TOHDOH, Naoki
; TITLE OF INVENTION: SINGLE-CHAIN ANTIBODY AGAINST HEPATITIS B VIRUS CORE
; TITLE OF INVENTION: PROTEIN, GENE THEREOF, AND THERAPEUTIC AGENT FOR
; TITLE OF INVENTION: HEPATITIS B CONTAINING THESE
; FILE REFERENCE: 0020-4682P
; CURRENT APPLICATION NUMBER: US/09/486,814A
; CURRENT FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 297

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;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6407214ris
;; STREET: One Liberty Place - 46th Floor
;; CITY: Philadelphia
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19103
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/587,526
;; FILING DATE:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/718,323
;; FILING DATE: 11-NO. 6407214-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Trujillo, Doreen Yanko
;; REGISTRATION NUMBER: 35,719
;; REFERENCE/DOCKET NUMBER: CARP-0054
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 568-3100
;; TELEFAX: (215) 568-3439
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 133 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-587-526-8

Query Match 75.5%; Score 447.5; DB 4; Length 133;
Best Local Similarity 76.3%; Pred. No. 1.2e-37;
Matches 87; Conservative 11; Mismatches 15; Indels 1; Gaps 1;

QY 1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNNMWRQNIKSLRWIGATIDPYVGTSY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVQLVQSGAEVKPGSSVKVSKASGYTFDTHMHWVRQAPGQGLEWIGTIDPETGGTAY 79
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDATVYIC-VSGMEYWGQTSVTYSS 113
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 NQKFKGRATLTADKSTNTAYMDLSLRSEDATVYICTVLRLMDYWGQTLVTYSS 133
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 15
US-07-634-278-57
; Sequence 57, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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;; APPLICATION NUMBER: US/07/634,278
;; FILING DATE: 19-DEC-1990
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/590,274
;; FILING DATE: 28-SEP-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/310,252
;; FILING DATE: 13-FEB-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/290,975
;; FILING DATE: 28-DEC-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 11823-002600
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 326-2400
;; TELEFAX: (415) 326-2422
;; INFORMATION FOR SEQ ID NO: 57:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 116 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-07-634-278-57

Query Match 75.1%; Score 445.5; DB 1; Length 116;
Best Local Similarity 73.3%; Pred. No. 1.6e-37;
Matches 85; Conservative 12; Mismatches 16; Indels 3; Gaps 1;

QY 1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNNMWRQNIKSLRWIGATIDPYVGTSY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVQSGAEVKPGSSVKVSKASGYTFDTHMHWVRQAPGQGLEWIGIYIPYNGGTGY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDATVYICVSG---MEYWGQTSVTYSS 113
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 NQKFKSRATITADESTNTAYMELSLRSEDATVYICARGRPAMDYWGQTLVTYSS 116
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Search completed: April 18, 2005, 10:07:36
Job time : 20 secs
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